Title: Perfect score: Sequence:

US-10-018-924-2\_COPY\_22\_146

ARLDVASEFRKKWNKWALSR......FTDKDKDNVAPRSKISPQGY

Š

protein

protein search, using sw model

Copyright

GenCore version (c) 1993 - 2002

5.1.3 Compugen Ltd.

October 17, 2002, 15:20:12;

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

```
No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Search time 8.55049 Seconds (without alignments) 357.079 Million cell updates/sec
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 14, Appli
Sequence 15, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 20, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 13, Appli
Sequence 2, Appli
                                                              Sequence 1, Application US/08233389C
Patent No. 5639855
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ANDRESCORD: O' STORE MEAUF
          Вþ
                            Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
US-08-233-389C-1
                                                         Best
                                                Matches
                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 125
CITY: New Y
STATE: NY
COUNTRY: US
ZIP: 10020
        22
ADDRESSEE:
                                             l Similarity
125; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New York
                                                                                                                                                                                                                                                                                                                                                                       E: c/o FISH & NEAVE
1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                           USA
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.0
10.0
9.9
9.9
9.9
9.9
9.9
9.7
9.7
9.7
9.5
                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           467
754
485
485
488
2485
2485
491
477
477
477
268
268
410
                                                                                                                                                                                                                                                      US/08/233, 389C
                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-945-574-1
US-08-941-262-1
US-08-941-262-3
US-08-453-956-15
US-08-452-930-15
US-08-452-930-15
PCT-US93-08.74-6
US-08-328-254-6
US-08-328-254-6
US-08-631-25
US-08-631-25
US-08-452-930-25
PCT-US93-08174-25
US-08-824-874-1
US-08-824-874-1
US-09-210-084-1
US-09-189-6278-10
US-09-189-6278-10
US-09-189-6278-10
                                          Score 655; DB 1;
Pred. No. 1e-72;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                            Version
                                                                                                                                                                                                                                                                            #1.
                                                              Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                           0;
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1, Appli
3, Appli
3, Appli
15, Appl
15, Appl
15, Appli
6, Appli
6, Appli
4, Appli
25, Appli
25, Appli
1, Appli
1, Appli
1, Appli
1, Appli
1, Appli
10, Appli
10, Appli
10, Appli
                                         0
```

Result No.

Query Match

Length

Description

SUMMARIES

is

11 12 13 14 15 15 16 17 17 18 19 19 22 23 23 23 24 27

100.0 100.0 100.0 100.0 100.0 93.3 93.3 93.3 93.3 10.3 110.3 110.3 110.3 110.3 110.0 110.0

US-08-233-389C-1
US-08-486-596A-1
US-08-486-596A-1
US-08-01-863-1
US-09-004-713-1
US-08-801-863-3
US-09-004-713-3
US-09-004-713-3
US-09-070-504-15
US-09-070-504-23
US-09-071-922A-14
US-09-011-922A-14
US-09-188-403-4
US-09-188-403-4
US-09-281-259-4
US-08-8170-180B-2
US-08-8170-180B-2
US-08-8170-180B-13
US-09-226-529-1
US-08-870-180B-13
US-09-226-529-13
US-09-236-529-13

Database

Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1,

2: /cgn2\_6/ptodata/1,

3: /cgn2\_6/ptodata/1,

4: /cgn2\_6/ptodata/1,

5: /cgn2\_6/ptodata/1,

6: /cgn2\_6/ptodata/1,

/cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/B\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/BCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

231628

231628 segs, 24425594 residues

Searched:

멍 Š

ş

```
US-08-801-863-]
                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-801-863-1
RESULT 3
US-08-486-596A-1
; Sequence 1, Application US/08486596A
; Patent No. 5837823
; GENERAL INFORMATION:
                                                                                                                                                      В
                                                                                                                                                                               Š
                                                                                                                                                                                                              Вþ
                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08801863 Patent No. 5830703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KITAMURA, Kazuo APPLICANT: KANGAWA, Kenji APPLICANT: MATSUO, Hisayuki APPLICANT: ETO, Tanenao TITLE OF INVENTION: ADRENOMED NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 596-9090 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                          TYPE: amino acids
TYPE: amino acid
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHEN-5 DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 SPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 SPQGY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: CONCUCASSIFICATION: 53
                                                                                                                           121 SPQGY 125
                                                                                                  142 SPQGY 146
                                                                                                                                                    22 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 81
                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                             1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONCURRENTLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADRENOMEDULLIN
                                                                                                                                                                                                                                                                                     100.0%; Score 655; DB 2
100.0%; Pred. No. 1e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/801,863
                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                      Length 185;
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                       Ωy
                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ρy
                                                                                                                                                                                                                                                                                                            밁
              COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                           22
```

Š

```
LENGTH: 185 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-486-596A-1
                                                                                                                                                                                                                                           US-09-004-713-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity luv.
125; Conservative
                                                                                                                                                                                         Sequence 1, Application US/09004713
Patent No. 5910416
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 596-90
TELEFAX: (212) 596-90
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY JAGENT INFORMATION:
NAME: HALEY Jr. James F.
REGISTRATION UNBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/486,596A
FILING DATE: JUNE 7, 1995
CLASSIFICATION: 530
CLASSIFICATION: 530
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ETO, Tal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                              APPLICANT: KITAM
APPLICANT: KANGA
APPLICANT: MATSU
APPLICANT: ETO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acid
                STREET: LACE
CITY: New York
CTATE: NY
                                                                                   TITLE OF INVENTION: ADRENOMEDULLIN NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1251 AV CITY: New York
                                                                                                                                                                                                                                                                                                     142 SPQGY 146
                                                                                                                                                                                                                                                                                                                                   121 SPQGY 125
                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                        ADDRESSEE:
10020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KITAMURA, Kazuo
KANGAWA, Kenji
MATSUO, Hisayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                        E: c/o FISH & NEAVE
1251 Avenue of the Americas
                                                                                                                                                   KANGAWA, Kenji
MATSUO, Hisayuki
                                                                                                                                                                                 KITAMURA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tanenao
                                                                                                                                     Tanenao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADRENOMEDULLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 655; DB 2; 100.0%; Pred. No. 1e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10
                                                                                                                                                                                 Kazuo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHGN-5 DIV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
```

Gaps

0

```
82 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                          ; MOLECULE TYPE: protein US-08-801-863-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-801-863-3
             Matches 114;
                            Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-233-389C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Applic
Patent No. 5830703
                                                                                                                                                    TELEFAX: (212) 596-9090 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 114; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: KITANURA, Kezuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, veCURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,863
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 530
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 596-9090 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 SPQGY 146
                                                                                                        TOPOLOGY:
                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 SPQGY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 ASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVADRSKI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 188 amino acids TYPE: amino acid TOPOLOGY: linear
                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : New York
                                                                                                                                                                                                                                                                                                                                                                                                                                               10020
                                                                                                                      : 188 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08801863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1251
           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Avenue of the Americas
                     93.3%;
91.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADRENOMEDULLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.3%;
   Score 611; DB 2; I
Pred. No. 2.6e-67;
8; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 611; DB 1;
Pred. No. 2.6e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                         Version #1.30
                                Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 188
     Indels
   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
```

RESULT 5 US-08-233-389C-3

Sequence 3, Application US/08233389C Patent No. 5639855

GENERAL INFORMATION:

APPLICANT:
APPLICANT:
APPLICANT:

KANGAWA, Kenji MATSUO, Hisayuki ETO, Tanenao

Tanenao

ADRENOMEDULLIN

KITAMURA, Kazuo

CORRESPONDENCE ADDRESS:

ADDRESSEE: C/C
ADDRESSEE: ACC

C/O FISH & NEAVE

Avenue of the Americas

TITLE OF INVENTION: NUMBER OF SEQUENCES:

STREET: 1251 AV CITY: New York STATE: NY

COUNTRY:

USA

10020

밁 Ş Вþ Ş Вb Qy

; MOLECULE TYPE: US-09-004-713-1

protein

TOPOLOGY:

amino acid

TELEFAX: (212) 596-909 INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acid

185 amino acids

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
NFORMATION FOR SEQ ID NO: 1:

ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHO

SHGN-5 DIV2 CON

APPLICATION NUMBER: US/09/00. FILING DATE: JANUARY 7, 1998 CLASSIFICATION: 435

US/09/004,713

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

MEDIUM TYPE:

Floppy disk

Query Match 100.08; Best Local Similarity 100.08;

22 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 81

1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60

Matches

125;

Conservative

0;

Score 655; DB 2 Pred. No. 1e-72; Mismatches

DB 2; Length 185; 0

Indels

Gaps

```
δÃ
1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
```

ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION UNMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5
TELECOMMUNICATION INFORMATION:

SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/233,389C

APPLICATION NUMBER: US/0: FILING DATE: 26-APR-1994 CLASSIFICATION: 530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,

밁

22

81

```
Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-486-596A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/486,596A
FILING DATE: JUNE 7, 1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV1
TELECOMMUNICATION INFORMATION:
TELEPAN: (212) 596-9000
TELEPAN: (212) 596-9090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
                                                                                                                                 S
                                                                                                                                                               밁
                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                          US-08-486-596A-3
                                                                            Š
                                                                                                          В
RESULT 8
US-09-004-713-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                     Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 SPQGY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 SPOGY 146
                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                     142 SPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: NY
                                                                               121 SPQGY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                              3, Application US/08486596A
5, 5837823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: c/o FISH & NEAVE
1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                   93.3%;
                                                                                                                                                                                                                     Score 611; DB 2; I
pred. No. 2.6e-67;
8; Mismatches 3;
                                                                                                                                                                                                                                                   Length 188
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                             0;
```

```
Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: 1i;
MOLECULE TYPE:
US-09-004-713-3
                                                                                                                                                                                                                                                                                                                           QΥ
                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                            US-09-070-504-14
                                                                                                                                                                                                                                             RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 591041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                          Sequence 14,
Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                               TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                    APPLICANT: Smith, Derek E APPLICANT: Saha, Shankar APPLICANT: Abel, Peter W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: JACCLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UZIP: 10020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                              142 SPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                               121 SPQGY 125
                                                                                                                                                                                                                                                                                                                                                                82 ASIPDAARIRVKRYROSMNNFOGLRSEGCREGTCTVOKLAHQIYOFTDKDKDGVAPRSKI 141
                                                                                                                                                                                                                                                                                                                                                                                  61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDKDNVAPRSKI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                  STREET:
                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09004713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                          4, Application US/09070504
6268474
Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                  E: Mueting, Raasch & Gebhardt, P.A.
119 No. 6268474th Fourth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                         Smith, Derek D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JANUARY 7, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.3%; Score 611; DB 2; 91.2%; Pred. No. 2.6e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIV2 CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>..</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
```

0;

COUNTRY:

Ņ

Gaps

1;

```
; MOLECULE TYPE: US-09-070-504-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 43.2%; Score 283; DB 4; Best Local Similarity 100.0%; Pred. No. 8.4e-28; Matches 52; Conservative 0; Mismatches 0;
                   TELEFAX: 514/JUL NO: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: 50 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
TELEPEAX: 612/305-1220
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McCormack, Myra H
                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                  TELEPHONE: 612/305-1220
                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Raasch & Gebhardt, |
STREET: 119 No. 6268474th Fourth Street
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Smith, Derek DappLICANT: Saha, Shankar APPLICANT: Abel, Peter W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                  REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 30-AP
                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                           CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 YRQSMNNEQGLRSFGCREGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 30-APR-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: McCormack, Myra H
REGISTRATION NUMBER: 36,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
                                                                                                                                               McCormack, Myra H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09070504
                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                               UMBER: US/09/070,504
30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Derek D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/09/070,504
                                                                                                                180.00020101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180.00020101
                                                                                                                                                                                                                                            Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                              RESULT 12
US-09-011-922A-3
                                                                                                                                      В
                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                   US-09-070-504-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-070-504-15
               Sequence 3, Application US/09011922A Patent No. 6320022 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-09-070-504-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       γ
                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
TELEFAX: 612/305-1228
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
      APPLICANT:
                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/070,504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: McCormack, Myra H
                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                             95 TYQKLAHQIYQFTDKDKDNVAPRSKISPQGY 125
                                                                                                                                                                                          Local 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                            1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Minneapolis
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 3
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23,
                                                                                                                                                                                              Similarity 100, 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McCormack,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3, Application US/09070504 6268474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Mueting, Raasch & Gebhardt, p.A.
119 No. 6268474th Fourth Street
Cuttitta, Frank; Martinez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saha, Shankar
Abel, Peter W.
                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                               peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-APR-1998
                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Derek D.
                                                                                                                                                                                                             24.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          муга
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.3%;
                                                                                                                                                                                              0,
                                                                                                                                                                                                             Score 163;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 231; DB 4; I
Pred. No. 1.9e-21;
Pred. No. 1.9e-31;
                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                          2.2e-1
                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                        Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 50;
                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
```

RESULT 10 US-09-070-504-15

Sequence 15, Patent No.

COUNTRY:

55401 M

0;

Gaps

0;

Дb δÃ

1

TOPOLOGY:

```
US-09-011-922A-3
                                                                                                                                                                                                                                                                    S
                                                                                                                                                      US-09-011-922A-14
                                                                                                                                                                                                                                   엉
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/011,922A
APPLICATION NUMBER: US/09/011,922A
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/002,514
FILING DATE: 18-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/002,936
FILING DATE: 30-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/013,172
APPLICATION NUMBER: US/60/013,172
APPLICATION DATA:
                                                                                        Sequence 14, Application US/09011922A Patent No. 6320022 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Karen; Ma
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: 1BM PC Compactible
OPERATING SYSTEM: MS WORD 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/I
FILING DATE: 16-Aug-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide HYPOTHETICAL: No
                                                         APPLICANT:
                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: P072
OTHER INFORMATION: PreproAM(116-146)
                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                             31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10154-0053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΝY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leslie A. Serunian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: MORGAN & FINNEGAN, L.L.P.
345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alfredo; Miller, Mae Jean; Unsworth, Edward
J.; Hook, William; Walsh, Thomas; Grey,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Karen; Macri, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASCII
                              Cuttitta, Frank; Martinez,
Alfredo; Miller, Mae Jean; Unsworth, Ed
J.; Hook, William; Walsh, Thomas; Grey,
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                    Karen; Macri,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Physiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adrenomedullin (AM) and the Gene-Related Product (PAMP) in Human Pathology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Functional Role of
                                                                                                                                                                                                                                                                                                                                 24.9%; Score 163; DB 4; 100.0%; Pred. No. 2.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT/US96/13286
                      Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97
                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2026-4202US3
                                                               Unsworth, Edward
                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                          Length 31
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                           0
```

```
Q
                                                                                                                                                                                                                                                                                                                                                                        US-09-011-922A-14
                                                                                                                                                                                                                                                밁
                                                                                                                                                                                     US-09-011-922A-7
                                                                                                                                                                                                  RESULT 14
                                                                                                                                               sequence 7, Application US/09011922A
Patent No. 6320022
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212) 751-68
INFORMATION FOR SEQ ID NO:
                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
COMPUTER: MS WORD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION DATE: 17-reu---
FILING DATE: 17-reu---
PRIOR APPLICATION NUMBER: US/60/002,514
APPLICATION NUMBER: 18-Aug-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/60/013,172
FILING DATE: 12-Mar-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13286
FILING DATE: 16-Aug-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: MS WORD SOFTWARE: ASCII CURRENT APPLICATION DATA:
           APPLICANT: J.; HOOK,
APPLICANT: Karen; ME
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 30-Aug-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10154-0053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 345 Par
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/60/002,936 FILING DATE: 30-Aug-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 17-Feb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                             OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                             l Similarity 100.
31; Conservative
ę
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leslie A. Seruni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: MORGAN & FINNEGAN, L.L.P.
345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
SEQUENCES
                                                                          Karen; Macri, Charles
                                                                                       Cuttitta, Frank; Martinez, Alfredo; Miller, Mae Jean; J.; Hook, William; Walsh, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                751-6849
                                                                                                                                                                                                                                                                                                           24.9%; suc
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Physiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adrenomedullin (AM) and the Gene-Related product (PAMP) in Human Pathology and
Physiology
17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/09/011,922A
                             Adrenomedullin (AM) and the Gene-Related product (PAMP) in Human Pathology and
                                                              Functional Role of
                                                                                                                                                                                                                                                                                                                                                                                          Synthetic homolog two-thirds of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35,353
                                                                                                                                                                                                                                                                                                                             Score 163; DB 4; pred. No. 2.2e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2026-4202US3
                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                 Thomas;
                                                                                             Unsworth, Edward
Thomas; Grey,
                                                                                                                                                                                                                                                                                                                                                                                              of
intact AM peptide
                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                   Length 31;
                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                       Gaps
```

0

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 Park Avenue

New York

```
RESULT 15
US-08-468-249A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: PAMP-20
OTHER INFORMATION:
OTHER INFORMATION:
US-09-011-922A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/08468249A
Patent NO. 5886148
GENERAL INFORMATION:
APPLICANT: Segre et al., Gino V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/011,922A FILING DATE: 17-Feb-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: US/60/002,514 FILING DATE: 18-Aug-1995 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/60/002,936 FILING DATE: 30-Aug-1995 PRIOR APPLICATION DATA: APPLICATION DA
                                                                                                                                                                          APPLICANT: Segre et al., Gino v.
TITLE OF INVENTION: PARATHYROID HORMONE
TITLE OF INVENTION: ENCODING SAME
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
71P: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/60/013,172
FILING DATE: 12-Mar-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13286
FILING DATE: 16-Aug-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS WORD 97
                                                                                                                         STREET:
CITY: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                  Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                   ΑM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10154-0053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leslie A. Serunian
RATION NUMBER: 35,353
                                                                                                                                           225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No
N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.3%; Sc. 100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proadrenomedullin N-
terminal 20 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 107; DB 4; Pred. No. 9.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2026-4202US3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                 RECEPTOR AND DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
```

```
Search completed: October 17, 2002, 15:22:03 Job time: 8.55049 secs
                                                                               В
                                                                                                                                                      В
                                                                                                                Ωy
                                                                                                                                                                                     QΥ
                                                                                                                                                                                                                                                                                                  US-08-468-249A-20
                                                                                                                                                                                                                                             Query Match
Best Local (
                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION NUMBER: US 07/681,702
PRIOR APPLICATION NUMBER: US 07/681,702
FILING DATE: 04-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/07100
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acids
                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                       525 ATTNGHSQLPGHAKPGA 541
                                                                                                                                      465 EVQAEIRKSWSRWTLALDFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPRLPP 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                  50
                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                         4 DVASEFRKKWNKWALSRG-KRELRM-SSSYP-----TGLADV--KAG---PAQTLIRP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/468,249A FILING DATE: 06-JUN-1995
                                                                                                            QDMKGASRSPEDSSPDA 66
                                                                                                                                                                                                                         25;
                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                   11.5%; Score 75; D
32.5%; Pred. No. 0.
tive 12; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      00786/071003
                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                   26;
                                                                                                                                                                                                                                                    Length 591;
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                               14;
                                                                                                                                                                                                             Gaps
```

Ş

THIS PACE BLAME (USOD)

```
October 17, 2002, 15:20:12; Search time 12.4495 Seconds (without alignments) 357.079 Million cell updates/sec
                                                                                                                                                                                                                  US-10-018-924-2_COPY_4_185
947
1 VSVALMYLGSLAFLGADTAR......SKPQAHGAPAPPSGSAPHFL 182
                                                                                                                                                                                                                                                                                                                                                                                                                           231628
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                            231628 segs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                 Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES

/cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/pcTUS\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/pcTUS\_COMB.pep:\*

5 :: .

Issued\_Patents\_AA:\*

Database :

	Description	Sequence 1, Appli	H	٦,	Sequence 1, Appli	'n	'n	Sequence 3, Appli	m	14,	Sequence 15, Appl	23,	3,	Sequence 14, Appl	7	7	Sequence 2, Appli	2,	ω	Sequence 5, Appli	10,	Sequence 10, Appl	10,	10,	10,	14,	15,	e' '9
	Desc	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec
SUMMARIES	ID	US-08-233-389C+1	US-08-801-863-1	US-08-486-596A-1	US-09-004-713-1	US-08-233-389C-3	US-08-801-863-3	US-08-486-596A-3	US-09-004-713-3	US-09-070-504-14	US-09-070-504-15	US-09-070-504-23	US-09-011-922A-3	US-09-011-922A-14	US-09-011-922A-7	US-09-390-721-2	US-08-949-637-2	US-09-291-488-2	US-08-444-734A-8	US-08-194-338-5	US-08-472-028A-10	US-09-071-296-10	US-09-196-268-10	US-09-015-683-10	US-09-191-998-10	US-09-039-198A-14	US-09-039-198A-15	US-08-486-839-6
	DB	П	7	7	7.	1	7	7	7	4	4	4	4	4	4	4	7	4	7	П	Н	4	4	4	4	4	4	7
	Query Match Length DB	185	185	185	185	188	188	188	188	25	20	31	31	31	20	401	496	496	450	450	490	490	490	490	490	373	373	387
ď	Query	100.0	100.0	100.0	100.0	86.3	86.3	86.3	86.3	29.9	24.4	17.2	17.2	17.2	11.3	9.1	8.4	8.4	8.3	8.2	8.1	8.1	8.1	8.1	8.1	8.0	8.0	8.0
	Score	947	947	947	947	817	817	817	817	283	231	163	163	163	107	86.5	80	80	79	78	76.5	76.5	76.5	76.5	76.5	92	92	9/
	Result No.	1	2	Ю	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27

Sequence 6, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 4, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli		
28 76 8.0 387 3 0S-09-151-011-6 29 76 8.0 410 1 0S-09-151-011-6 30 76 8.0 410 1 0S-09-43-623-6 31 76 8.0 466 2 0S-08-486-899-4 33 76 8.0 466 3 0S-09-151-011-4 34 76 8.0 466 4 0S-09-039-198A-2 35 75 8.0 466 4 0S-09-039-198A-2 36 75 7.9 931 4 0S-09-039-198A-2 37 74.5 7.9 933 4 0S-08-980-115-14 38 74.5 7.9 933 4 0S-08-980-115-14 39 74.5 7.9 933 4 0S-08-980-115-14 40 74 7.8 302 2 0S-08-893-85-3 41 73.5 7.8 1323 1 0S-08-013-3 41 73.5 7.6 434 1 0S-08-036-138E-4 42 72 7.6 434 1 0S-08-939-366-6	ALIGNMENTS	RESULT 1 US-08-233-389C-1 US-08-233-389C-1 Sequence 1, Application US/08233389C Patent No. 5639855 GENERAL INFORMATION: APPLICANT: KITAMURA, Kazuo APPLICANT: KANGAWA, Kenli APPLICANT: ANGAWA, Kenli APPLICANT: ETO, Tanenao TITLE OF INVENTION: ADRENOMEDULLIN NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEE: C/O FISH & NEAVE STREET: 1251 Avenue of the Americas CITY: New York STRATE: NY COUNTRY: USA IP 10020 COMPUTER: IBP PC Compatible OPERATING SYSTEM: PC-DOS/NS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/233,389C FILING DATE: 26 AAPR-1994 CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION: NAME: HALEY JT. James REGISTRATION NUMBER: S17,794 REFERENCE/DOCKET NUMBER: S17,794 REFERENCE/DOCKET NUMBER: S7,794 REFERENCE/DOCKET NUMBER: S17,794 REJERENCE/DOCKET NUMBER: S17,794 REJERENCE/DOCKET NUMBER: S17,794 REJERENCE/DOCKET

Gaps Query Match
100.0%; Score 947; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 4.9e-99;
Matches 182; Conservative 0; Mismatches 0; Indels

δλ g

ö

; 0

184 FL 185

g

RESULT 3

```
ö
 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
              121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAPH 180
                                                                              61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAPH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 947; DB 2; Length 185; 100.0%; Pred. No. 4.9e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM FC compatible
OPPERTY. SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,863
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHGN-5 DIV3
                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
ATTORREY/AGENT INFORMATION:
NAME: HALEY JT., James F.
REGISTRATION NUMBER: 27,794
REPRENCE/DOCKET NUMBER: SHGN-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                       Sequence 1, Application US/08801863
Patent No. 5830703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 185 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.0
Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10020
                                                                                                                                               ||
FL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FL 182
                                                                                                                            FL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-801-863-1
                                                                                                                                                                                                                         US-08-801-863-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
61
                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                          RESULT 2
                               g
                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
à
                                                               à
                                                                                                                            à
                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAPH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 947; DB 2;
100.0%; Pred. No. 4.9e-99;
ive 0; Mismatches 0;
                                                                                                                                                                                                                         E: c/o FISH & NEAVE
1251 Avenue of the Americas
                                                                           APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAMA, Kenj1
APPLICANT: MATSUO, HISAJUK1
APPLICANT: ETO, TANGAGO
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,596A
FILING DATE: JUNE 7, 1995
CLASSIFICATION: 530
                 Sequence 1, Application US/08486596A Patent No. 5837823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09004713; Patent No. 5910416
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: . KANGAWA, Kenji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                  New York
                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 10020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||
| FL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 FL 182
US-08-486-596A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-486-596A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-004-713-1
                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                  CITY: N
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 IYQFTDKDKDNVAPRSKISPQGYGRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.3%; Score 817; DB 1; Length 188;
89.1%; Pred. No. 2.2e-84;
1ve 10; Mismatches 9; Indels
         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBP Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,389C
FILING DATE: 26-APR-1994
CLASSIFICATION NUMBER: US/08/233,389C
FILING DATE: 26-APR-1994
CLASSIFICATION NUMBER: ST,794
REFERENCE/DOCKET NUMBER: 77,794
REFERENCE/DOCKET NUMBER: 77,794
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 21,794
REFERENCE/DOCKET NUMBER: SHGN-5
TELEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9000
SEQUENCE CHARACTERISTICS:
TENGTH 188 AMINO acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STAIL.
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/801,863
TITING DATE: CONCURRENTLY HEREWITH
FROM THE CONCURRENT FOR THE CONCUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08801863
Patent No. 5830703
Patent No. 5830703
Patent No. 5830703
Patent No. 5830703
Patent No. 5830708
PAPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 188 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 89.1%
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-233-389C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAPH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 100.0%; Score 947; DB 2; Length 185; Best Local Similarity 100.0%; Pred. No. 4.9e-99; Matches 182; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,713
FILING DATE: JANUARY 7, 1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHGN-5 DIV2 CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08233389C
Patent No. 5639855
GENERAL INFORMATION:
APPLICANT: RITAMURA, Kazuo
APPLICANT: RANGAWA, Kenji
APPLICANT: RANGAWA, Kenji
APPLICANT: BTO, Tanenao
INVENTION: PTO, Tanenao
INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                     ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INRORAMITON:
NAME: HALEY JI., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
INFORMATION FOR SEC ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 185 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                   CITY: New York
                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 FL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-08-233-389C-3
                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-004-713-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                  US-09-004-713-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                         δ
                                                                                                                                                                                           g
                                                 g
                                                                                     ò
                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                          61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                                                                                                                                                                                                                                                                                                                             64 AQTVIRPQDVKGSSRSPQASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                       4 VPVALMYLGSLAFLGADTARLDVAAEFRKWNKWALSRGKRELRLSSSYPTGIADLKAGP 63
                                                                                                                                                                                                                                                                    1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 188;
                                                                                                                                                                                               Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 86.3%; Score 817; DB 2; Length 16
Best Local Similarity 89.1%; Pred. No. 2.2e-84;
Matches 156; Conservative 10; Mismatches 9; Indels
                                                                                                                                                                                             86.3%; Score 817; DB 2; Length 18
89.1%; Pred. No. 2.2e-84;
Live 10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FOLGY disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGFWARE: Patentin Release #1.0, Version #1.30
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,596A
FILING DATE: JUBER: US/08/486,596A
FILING DATE: JUBER: US/08/486,596A
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: SHOW
REGISTRATION NUMBER: SHOW
TELEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9000
TELEPAX: (212) 596-9000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: KANGAWA, Kenji
APPLICANT: WATSIO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08486596A Patent No. 5837823
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amilio acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KITAMURA, Kazuo
                                                                                                                                                                                                                Similarity 89.19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                          , MOLECULE TYPE: protein US-08-801-863-3
                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                     Query Match
Best Local Simi
Matches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-486-596A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-486-596A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: N
                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                  원
```

```
61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 AQTVIRPQDVKGSSRSPQASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                      64 AQTVIRPQDVKGSSRSPQASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 100.4
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible.
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,713
FLING DATE: JANUARY 7, 1998
TLING DATE: JANUARY 7, 1998
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: SHGN-5 DIV2 CON
TELEFHONE: (212) 596-9000
TELEFHONE: (212) 596-9000
TELEFAX: (212) 596-9000
TELEFAX: (212) 596-9000
TOWNEY THE SEQUENTION OF SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.3%; Score 817; DB 2; I
ilarity 89.1%; Pred. No. 2.2e-84;
Conservative 10; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: C/O FISH & NEAVE STREET: 1251 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                   APPLICANT: KITAMORA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                    Sequence 3, Application US/09004713
Patent No. 5910416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-09-004-713-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 156; Conserv
```

Ų

```
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Smith, Derek D.
APPLICANT: Shai, Shankar
APPLICANT: Shai, Shankar
APPLICANT: Abal, Peter W.
TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Mueting, Raasch & Gebhardt, P.A.
STREET: 119 No. 6268474th Fourth Street
CITY: Minneapolis
STATE: MN
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 50;
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,504
FILING DATE: 30-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCCORMACK, MYTA H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET UNBER: 36,602
REFERENCE/DOCKET UNBER: 180.00020101
TELEPHONE: 612/305-1220
TELEPHONE: 612/305-1220
TELEPHONE: 612/305-1220
TELEPHONE: G12/305-1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/09/070,504
FILING DATE: 30-APR-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 24.4%; Score 231; DB 4; L
Best Local Similarity 84.6%; Pred. No. 3.8e-19;
Matches 44; Conservative 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180.00020101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23, Application US/09070504 Patent No. 6268474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MCCAFMECK, Myra H
REGISTRATION NUMBER: 36,602
REPRENCE/DOCKET NUMBER: 180.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-070-504-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: peptide US-09-070-504-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-070-504-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/09070504
Fatent No. 6268474
GENERAL INFORMATION:
APPLICANT: Smith, Derek D.
APPLICANT: Saha, Shankar
APPLICANT: Abel, Peter W.
ITYLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
ITYLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Mueting, Raasch & Gebhardt, P.A.
STREET: 119 No. 6268474th Fourth Street
CITY: Minneapolis
STATE: M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-070-504-15

Sequence 15, Application US/09070504

Sequence 15, Application US/09070504

Patent No. 6268474

GENERAL INFORMATION:
APPLICANT: Saha, Shankar

APPLICANT: Saha, Shankar

APPLICANT: Abel, Peter W.

TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR

TITLE OF INVENTION: SUPERFRAMILY AND METHODS OF USE

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.

STREET: 119 No. 6268474th Fourth Street

CITY: Minneapolis

CONTY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 29.9%; Score 283; DB 4; Length 52; Best Local Similarity 100.0%; Pred. No. 5.6e-25; Matches 52; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,504
FILING DATE: 30-APR-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180.00020101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: MCCOTMACK, Myra H
REGISTATION UNDBER: 36,602
REFERENCE/DOCKET NUMBER: 180.0
TELECOMMUNICATION INFORMATION:
TELEFAX: 612/305-1220
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 52 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide US-09-070-504-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MN
                            US-09-070-504-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
```

Gaps

```
APPLICANT: Cuttitta, Frank; Martinez,
APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
APPLICANT: A.; Hook, William; Walsh, Thomas; Grey,
APPLICANT: Karen; Marti, Charles of
TITLE OF INVENTION: Functional Role of
TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
TITLE OF INVENTION: Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic homolog of two-thirds of the intact AM peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.2%; Score 163; DB 4; 100.0%; Pred. No. 9.2e-12; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS WORD 97
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,922A
FILING DATE: 17-Feb-1998
FILING DATE: 18-Aug-1995
PRIOR APPLICATION NDATA:
APPLICATION NUMBER: US/60/002,514
FILING DATE: 30-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/013,172
FILING DATE: 12-Mar-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/013,172
FILING DATE: 12-Mar-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/013,172
FILING DATE: 16-Mar-1996
ATTICNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 143
    113 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 143
                         1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TVOKLAHOIYQETDKDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEE: MORGAN & FINNEGAN, L.L.P. : 345 Park Avenue
                                                                                                                                                        Sequence 14, Application US/09011922A Patent No. 6320022 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Leslie A. Serunian
REGISTATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPANE: (212) 758-4800
TELEPAX: (212) 758-4800
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 17.2
Best Local Similarity 100.
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTHER INFORMATION:
COTHER INFORMATION:
US-09-011-922A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
STREET: 34
                                                                                                                   RESULT 13
US-09-011-922A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                   ö
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                   ö
                                                                                                                                                                                                                                                                                                                   APPLICANT: Cutilita, Frank; Martinez,
APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
APPLICANT: A.; Hook, William; Walsh, Thomas; Grey,
APPLICANT: Karen; Macri, Charles
TITLE OF INVENTION: Functional Role of
TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
TITLE OF INVENTION: Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: 17
    Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 31;
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
17.2%; Score 163; DB 4; I
100.0%; Pred. No. 9.2e-12;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.2%; Score 163; DB 4; I
ilarity 100.0%; Pred. No. 9.2e-12;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/60/002,514
FILING DATE: 18-aug-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/002,936
FILING DATE: 30-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/013,172
FILING DATE: 12-MAT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DCT/US96/13286
FILING DATE: 16-Aug-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lesalle A. Serunian
REGISTRATION NUMBER: 35,33
REFERENCE/DOCKET NUMBER: 35.33
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
                                                                                           113 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: P072
; OTHER INFORMATION: PreproAM(116-146)
US-09-011-922A-3
                                                                                                                     1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MORGAN & FINNEGAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/011,922A
FILING DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                 Sequence 3, Application US/09011922A
Patent No. 6320022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS WORD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 345 Park Avenue
New York
    Query Match 17.2'
Best Local Similarity 100.
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
STREET: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: NY
                                                                                                                                                                                                                                 US-09-011-922A-3
                                                                                                à
                                                                                                                                        g
```

Gaps ö

Indels

Length 31;

```
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                        GENERAL INFORMATION:
APPLICANT: OLITitia, Frank; Martinez,
APPLICANT: Alfredo, Miller, Mae Jean; Unsworth, Edward
APPLICANT: Alfredo, Miller, Mae Jean; Unsworth, Edward
APPLICANT: Alfredo, Milliam; Walsh, Thomas; Grey,
APPLICANT: Karen; Macri, Charles
TITLE OF INVENTION: Functional Role of
TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
TITLE OF INVENTION: Physiology
NUMBER OF SEQUENCES:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.3%; Score 107; DB 4; Length 20; 100.0%; Pred. No. 1e-05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 16-ANG-1996
ATTORNEY_AGENT INFORMATION:
NAME: Leslie A. Serunian:
REGISTRATION NUMBER: 35,353
FRETERENCE_DOCKET NUMBER: 35,353
TELECOMMUNICATION INFORMATION:
TELEPAN: (212) 751-6849
INFORMATION FOR SEQ ID NO: 7:
INFORMATION FOR SEQ ID NO: 7:
LEGETH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: Proadrenomedullin N-
CTHER INFORMATION: · terminal 20 peptide
US-09-011-922A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,922A
FILIN DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/002,514
FILIND DATE: 18-Aug-1995
PRIOR APPLICATION DATA: 30-Aug-1995
PRIOR APPLICATION NUMBER: US/60/002,936
FILING DATE: 30-Aug-1995
PRIOR APPLICATION NUMBER: US/60/013,172
FILING DATE: 12-Mai-1996
PRIOR APPLICATION DATA: 1996
PRIOR APPLICATION DATA: 1996
PRIOR APPLICATION DATA: 1996
PRIOR APPLICATION DATA: 1997
FILING DATE: 12-Mai-1996
PRIOR APPLICATION DATA: 1996
PRIOR APPLICATION DATA: 1996
PRIOR APPLICATION DATA: 1997
FILING DATE: 12-Mai-1996
PRIOR APPLICATION DATA: 1997
FILING DATE: 12-Mai-1996
FRIOR APPLICATION DATA: 16-Mai-1996
FRIOR APPLICATION DATA: 19-Mai-1996
F
                                                                        Sequence 7, Application US/09011922A
Patent No. 6320022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS WORD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: PAMP-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE:
                                  US-09-011-922A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
RESULT 14
```

Gaps

ö q

```
APPLICANT: STUTZAAN-ENGWALL, KIM J.
APPLICANT: STUTZAAN-ENGWALL, KIM J.
APPLICANT: PRICE, BRENDA S.
TITLE OF INVENTION: STREPTOMYCES AVERMITILIS REGULATORY GENES FOR INCREASED TITLE OF INVENTION: AVERMECTIN PRODUCTION
FILE REFERENCE: PC9944A
CURRENT APPLICATION UNDRABE: uS/09/390,721
CURRENT FILING DATE: 1999-09-07
BARLIER APPLICATION NUMBER: 60/100,134
EARLIER FILING DATE: 1998-09-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 ERLRIARELHDVVTHSMGLIAVKVGVANHVLHIRPQEAYDALQVIERTSRTALN-DMRRM 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 LGVLRTSEGEROSAALGPLPGALALPDLVGQAGAQLTMRGVESLPDGVALAVYRIVQEAL 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 SPGLLLLGFRAALLGA--------WOLGRAARQRRAFAVRAAEQLAQRAVTE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 ------SYPTGLADVKAGPAQTL--IRPQDMKGASRSPEDSSPDAARIRVKRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.1%; Score 86.5; DB 4; Length 401; Best Local Similarity 20.5%; Pred. No. 0.12; Matches 52; Conservative 26; Mismatches 83; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 SVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 DNVA-----PRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 RQSMNNFQGLR---SFGCRFGTCTVQKLAHQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: October 17, 2002, 15:22:04
Job time : 13.4495 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT CRGANISM: Streptomyces avermitilis US-09-390-721-2
RESULT 15
US-09-390-721-2
; Sequence 2. Application US/09390721
; Patent No. 6197591
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 ---APAPPSGSAPH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379 FAAGPRPEGGFAVH 392
```

THIS PAGE BLANK (USSTO)

<u>.</u>.

.

```
October 17, 2002, 14:45:20 ; Search time 4.53865 Seconds (without alignments) 279.848 Million cell updates/sec
                                                                                                                                                                                 US-10-018-924-2_COPY_95_146
283
1 YRQSMNNFQGLRSFGCRFGT......FTDKDKDNVAPRSKISPQGY 52
                                                                                                                                                                                                                                                                                                                                                                       231628
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                      231628 seqs, 24425594 residues
                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                 Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                        Run on:
```

Issued\_Patents\_AA:\*
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\* Database

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 14, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 15, Appli Sequence 15, Appli Sequence 17, Appli Sequence 17, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli
SUMMARIES	US-09-070-504-14 US-08-233-389C-1 US-08-808-801-863-1 US-08-486-596A-1 US-08-486-596A-3 US-08-004-713-3 US-08-009-004-713-3 US-08-09-004-713-3 US-09-001-922A-14 US-09-011-922A-14 US-09-011-922A-14 US-09-011-922A-14 US-09-011-922A-14 US-09-011-922A-14 US-09-011-922A-14 US-09-011-922A-14 US-09-011-922A-14 US-08-168-16-18 US-08-168-16-18 US-08-168-404-4 US-08-91-942G-5 US-08-91-222-17
Length DB	185 1 1885 2 1885 2 1885 2 1888 1 1888 2 188
% Query Match L	1000.0 10000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1
Score	28833 28833 28833 20077777 2003 2003 2003 2003 2003 200
Result No.	10848978801111111111111111111111111111111111

; 0 52 52

g ö

Appl Appl Appl Appl Appl Appl Appl Appl		0;
933,		Gaps
sednence sed		:0
nbess		52; s
	B GC BPT	Length
	CGRP-RECEPTOR OF USE A.	
9-207 -621-17 88-532 818-17 9-231-797-17 98-934-224-17 88-934-223-17 9-413-492-17 9-413-492-17 9-413-492-17 9-413-492-17 9-413-492-17 9-413-492-17 9-731C-10 88-290-731C-2 8-290-731C-2 8-290-731C-6 8-290-731C-6 8-290-731C-6 8-290-731C-6	OF CG OOF CG OOF H.1	DB 4
-621 -818 -797 -224 -843 -813 -731 -731 -731 -731 -731 -731	MENTS OF METHOD ABITOR VERSION VERSION	283; No. 8e
9-120 9-	ALIGNMENTS 0504 ANTAGONISTS OF ( ILY AND METHODS (s Gebhardt, P., Fourth Street S-DOS #1.0, Version ( 070,504	۸ . 5
US-09-207- US-08-532- US-08-231- US-08-934- US-08-934- US-08-934- US-08-138- US-08-290- US-08-290- US-08-290- US-08-290- US-08-290- US-08-290- US-08-290- US-08-290- US-08-260- US-08-260- US-08-260- US-08-956- US-08-956- US-08-956- US-08-956- US-08-956- US-08-956- US-08-956- US-08-956- US-08-956- US-08-956- US-08-956- US-08-956- US-08-956- US-08-956- US-08-956-	AANT ILY Four \$1.000	Sc. Pr
0000004441000000001000	arek D.  In US/0907  In I	.08;
10 10 10 10 10 10 10 10 10 10 10 10 630 630 630 430 435	Pplication US/0907 4474 AATON: Smith, Derek D. Saba, Shankar Abab, Peter W. ENTION: SUPERFAM CURNCES: 23 CE ADDRESS: Mucting, Raasch Mucting, Raasch 19 No. 6268474th neapolis DABLE FORM: E: Floppy disk IBM PC compatibl. SYSTEM: E: Floppy disk IBM PC compatibl. SYSTEM: NUMBER: US/09/W PATENTION: NUMBER: US/09/BE: 30-APR-1998 TION: STATION: NUMBER: US/09/BE: 30-APR-1998 TION: SUMBER: US/09/BE: US/	100. 100. 1ve
н ннн	olication ( YITA)  MITAN Smith, Dere Smath, Dere Shank Mueting, Hueting, Hueti	:y ervat
18.0 18.0 18.0 18.0 18.0 18.0 17.7 17.7 17.7 17.7 17.7 17.7 17.3	4-14 4. Applicatio 6268474 WT: Smith, D WT: Shaw, Shaw	Similarity 100 2; Conservative
551 551 551 550 550 550 550 550 550 550	4-14 4, App 62684 62684 NT: S	Simi 2;
47	SEGULT 1 Sequence 14, Application US/0907 Patent No. 6266474 Sequence 14, Application US/0907 Patent No. 6266474 APPLICANT: Saha, Shankar APPLICANT: Saha, Shankar APPLICANT: Saha, Shankar APPLICANT: Saha, Shankar APPLICANT: Shankar APPLICANT: Saha, Shankar APPLICANT: Saha, Shankar APPLICANT: Saha, Shankar TITLE OF INVENTION: SUPERFAM NUMBER: OF SEQUENCE: 23 CORRESPONDENCE ADDRESS: ADDRESSES: Mucting, Raasch STREET: 119 NO. 6268474th CITY: Minneapolis STREET: 119 NO. 6268474th CITY: Minneapolis STREET: 105401 COMPUTER: EMADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OFFATING SYSTEM: PC-005/MS SOFTWARE: PALENTIN PC-005/MS CLASSIFICATION UNMBER: US/09/ FILING DATE: 30-APR-1998 CLASSIFICATION NAME: MCCOTMACK, MyTA H REGISTRATION NUMBER: 36,60; RERERENCE/DOCKET NUMBER: 36,60; TELEPHONE: 612/305-1220 TELEFAX: CHARACTERISTICS: LEMETRY: 22 amino acids TYPE: amino acids TYPE: amino acids TYPE: peptide, TYPE: Peptide,	ial
288 444 444 443 454 454 454 454 454 454 454	SULT 1 -09-070- Sequence Sequence APPLI CONN CONN CONN CONN CONN APPLI A	Query Ma Best Loc Matches
	RESULT Sequence of	On Ma

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER KEALABLE FURN.

COMPUTER ELPOPPY disk
COMPUTER: IBM PC Compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,596A
FILING DATE: JUNE 7, 1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY JF., James F.
REGISTRATION NUMBER: SHGN-5 DIVI
TELEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9000
INFORMATION FOR SEG ID NO: 1:
SEQUENCE CHARACTERISTICS:
CENTRAL 185 amino Acids
COMPUTER: 1BM FC COMPUTER: 0879TEM: PC-DOS/MS-DOS
SOPTWARE: PACENTIN RC-DOS/MS-DOS
SOPTWARE: PACENTIN RC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,863
FILING DATE: COMCURRENTLY HEREMITH
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
TELEPHONE: (212) 596-9000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CARRACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acids
TYPE: amino acid
TYPE: APPLICATION INFORMATION:
TOPOLOGY: 11near
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 283; DB 2;
Best Local Similarity 100.0%; Pred. No. 3.8e-34;
Matches 52; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08486596A
Patent No. 5837823
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenli
APPLICANT: ATTO, Tanenao
TITLE OF INVENTION: ADENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: c/o FISH & NEAVE
1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10020
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1251
CITY: New YC
STATE: NY
COUNTRY: US/
ZIP: 10020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
US-08-486-596A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-801-863-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/233,389C
FILING DATE: 26-APR-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 283; DB 1;
illarity 100.0%; Pred. No. 3.8e-34;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MESULT 3
US-08-801-863-1
Sequence 1, Application US/08801863
PRACENT NO SB30703
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KATAMARA, Kanji
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: APRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Average
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: C/O FISH & NEAVE
1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                          ADDRESSEE: C/O FISH & NEAVE STREET: 121 Avenue of the Americas CITY: New York STATE: NY
                                                                                                                                                       APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGANA, Kenjl
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITILE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                     Sequence 1, Application US/08233389C Patent No. 5639855 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 185 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 52; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                     USA
10020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-233-389C-1
```

Query Match

COUNTRY:

185 amino acids amino acid

TOPOLOGY:

US-08-486-596A-1

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

USA 10020

COUNTRY: CITY: N STATE:

Query Match

```
1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 188;
                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,389C
FILING DATE: 26-APR-1994
CLASSIFICATION: 530
ATTORNEY/AGRYT INFORMATION:
NAME: HALLEY Jr., James F.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
RECENENCE/DOCKET NUMBER: 27,794
TELEPHONICATION INFORMATION:
TELEPHONICATION INFORMATION:
TELEPHONE: (212) 596-9000
INFORMATION FROM SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 anino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 97.9%; Score 277; DB 1; Best Local Similarity 98.1%; Pred. No. 3e-33; Matches 51; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INCENTATION US/08801863
GENERAL INFORMATION
APPLICANT: KITAMURA, KAZUO
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10020
COMPUTER PROFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
TELECOMMUNICATION INFORMATION:
TELERONE: (212) 596-9000
TELEROX: (212) 596-9000
INFORMATION FOR SEQ ID NO: 3:
                1251 Avenue of the Americas
                                                        STATE: NY
COUNTRY: USA
ZIP. 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/801,863
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                       New York
                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-801-863-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                              Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 185;
                                                                                    1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: U.SA.

2 IP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/004,713
FILING DATE: JANUARY 7, 1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HALEY JI., James F.
REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION S96-9090
TELEFRANCE: (212) 596-9090
TELEFRANCE: (212) 596-9090
INFORMATION FOR SEQ ID NO: 1:
100.0%; Score 283; DB 2;
100.0%; Pred. No. 3.8e-34;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 100.0%; Score 283; DB 2; Best Local Similarity 100.0%; Pred. No. 3.8e-34; Matches 52; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                     Sequence 1, Application US/09004713
Patent No. 5910416
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ATSUO, Hisayuki
APPLICANT: TTO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KITAMORA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, HISAYUKI
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NOMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08233389C
Patent No. 5639855
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 185 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-004-713-1
                  Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-233-389C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: N
                                                                                                                                                                                                                         US-09-004-713-1
                                                                                                                                                                                                  RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

ö

Gaps

.; 0

```
USA
                                                                                                                                                                        COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                         CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 277; DB 2; Length 188;
Pred. No. 3e-33;
0; Mismatches 1; Indels
                                                                                                                      Ouery Match 97.9%; Score 277; DB 2; Length 188; Best Local Similarity 98.1%; Pred. No. 3e-33; Matches 51; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

COMPUTER: FLORPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,596A

FILING DATE: JUNE 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: HALEY IT., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIVI
TELEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08486596A
Patent No. 5837823
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANY: MATSUO, Hisayuki
APPLICANY: TO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09004713 Patent No. 5910416 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.9%;
illarity 98.1%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KITAMURA, Kazuo
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-801-863-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-486-596A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NY COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                      US-08-486-596A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-004-713-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                  à
                                                                                                                                                                                                                                g
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDKVAVAPRSKISPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-070-504-15
Sequence 15, Application US/09070504
Sequence 15, Application US/09070504
GENERAL INFORMATION:
APPLICANT: Smith, Derek D.
APPLICANT: Saha, Shankar
APPLICANT: Abel, Peter W.
TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
NUMBER OF SEQUENCES: 23
NUMBER OF SEQUENCES: 23
ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPUTER: BATCHILIN Release #1.0, Version #1.30
SOFTWARE: Patchilin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/070,504
FILLING DATE: 30-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,713
FILING DATE: JANUARY 7, 1998
CLASSIFICATION: 435
ATTORNEY/AGBWT INFORMATION:
NAME: HALEY JT., James F.
REGISTRATION NUMBER: SHGN-5 DIV2 CON
TELECOMMUNICATION INDER: 3600000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ....oureSSE: ...oureSS: ...oureSSE: ...our
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 277; DB 2;
Pred. No. 3e-33;
0; Mismatches
APPLICANT: MATSUO, HISAYUKI
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: -/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 188 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear;
MOLECULE TYPE: protein
US-09-004-713-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 51; Conserv
```

```
GENERAL INFORMATION:
APPLICANT: Cuttitta, Frank; Martinez,
APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
APPLICANT: Tracen; Macri, Charles
APPLICANT: Karen; Macri, Charles
TITLE OF INVENTION: Functional Role of
TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
TITLE OF INVENTION: Product (PAMP) in Human Pathology and
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
COMPUTER: ASCII

SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,922A
FILING DATE: 17-Feb-1998
FILING DATE: 18-409-1995
FILING DATE: 18-409-1995
FILING DATE: 30-409-1995
FILING DATE: 30-409-1995
FILING DATE: 30-409-1995
FILING DATE: 10-A09-1995
FILING DATE: 10-A09-1996
FILING DATE: 12-Mar-1996
FILING DATE: 12-Mar-1996
FILING DATE: 12-Mar-1996
FILING DATE: 16-A09-1996
ATTORNEY FAGENT INFORMATION:
ANAWE: 1-A01-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TVQKLAHQIYQFTDKDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
US-09-011-922A-3
  1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                                                              Sequence 3, Application US/09011922A
Patent No. 6320022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Leslie A. Serunian
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 57.6%
Best Local Similarity 100.0
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . peptide
No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                               US-09-011-922A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YRQSMN--QGSRSTGCRFGTCTMQKLAHQIYQFTDKDKDKDGMAPRNKISPQGY 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 57.6%; Score 163; DB 4; Length 31; Best Local Similarity 100.0%; Pred. No. 2.2e-17; Matches 31; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23, Application US/09070504

Patent No. 6268474
GENERAL INFORMATION:
APPLICANT: Saha, Shankar
APPLICANT: Saha, Shankar
APPLICANT: Abel, Peter W.
TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                       Score 231; DB 4; Length 50; Pred. No. 3.6e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/09/070,504
FILING DATE: 30-APR-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSE: Mueting, Raasch & Gebhardt, P.A.
STREET: 119 No. (568474th Fourth Street
CITY: Minneapolis
NAME: MCCOTMack, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180.00020101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1228
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: MCCOrmack, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180.00020101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 612/3UD-1120
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
TENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                          81.6%;
84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                           44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-070-504-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-070-504-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-070-504-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

ö Gaps ö 57.6%; Score 163; DB 4; Length 31; 100.0%; Pred. No. 2.2e-17; ive 0; Mismatches 0; Indels

RESULT 13

```
APPLICANT: Cuttitta, Frank; Martinez,
APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
APPLICANT: Karen; Macri, Charles
TITLE OF INVENTION: Functional Role of
TITLE OF INVENTION: Addrenomedullin (AM) and the Gene-Related
TITLE OF INVENTION: Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: YGG-Preproam (122-131)
US-09-011-922A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTURNEL/ADEAL AND CONTROLL AND CONTROLL AND NAME: LESTIE A. SETUTION NUMBER: 35,353
RECISTRATION NUMBER: 2026-4202US3
REFERENCE/DOCKET NUMBER: 2026-4202US3
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
SCETMARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,922A
FILING DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/002,514
FILING DATE: 18-Aug-1995
PRIOR APPLICATION NUMBER: US/60/002,936
FILING DATE: 30-Aug-1995
PRIOR APPLICATION NUMBER: US/60/013,172
FILING DATE: 12-Mar-1996
PRIOR APPLICATION NUMBER: US/60/013,172
FILING DATE: 12-Mar-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13286
FILING DATE: 16-Aug-1996
ATTORNEY/AGENT INFORMATION:
NAME: Leslie A. Serunian
                                                                                                                                                                                                                                                                     MORGAN & FINNEGAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                         STATE: NY
COUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS WORD 97
                                                                                                                                                                                                             NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNE
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 20.1
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 HQIYQFTDKD 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 HQIYQFTDKD 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                  Sequence 14, Application US/09011922A

Betant No. 6320023

GENERAL INFORMATION:
APPLICANT: Cuttitta, Frank; Martinez,
APPLICANT: Alfredo: Miller, Mae Jean; Unsworth, Edward
APPLICANT: J. Hook, William; Walsh, Thomas; Grey,
APPLICANT: Karen: Macri, Charles
TITLE OF INVENTION: Functional Role of
TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
TITLE OF INVENTION: Product (PAMF) in Human Pathology and
TITLE OF INVENTION: Physiology
NUMBER OF SEQUENCES: 17
CORRESPONDEMCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 57.6%; Score 163; DB 4; Length 31; Best Local Similarity 100.0%; Pred. No. 2.2e-17; Matches 31; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic homolog of two-thirds of the intact AM peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COTACAL TAPLALCATION DATA:
APPLICATION NUMBER: US/09/011,922A
FILING DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/002,514
FILING DATE: 18-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/002,936
FILING DATE: 30-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/013,172
FILING DATE: 12-Mar-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/013,172
FILING DATE: 11-Mar-1996
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 16-Mug-1996
ATPONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2026-4202US3
                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: MORGAN & FINNEGAN, L.L.P. STREET: 345 Park Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS WORD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Leslie A. Serunian
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 20;
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10154-0053
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
CTHER INFORMATION:
US-09-011-922A-14
US-09-011-922A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

```
RESULT 15
US-08-265-628-2
'Sequence 2, Application US/08265628
'Sequence 2, Application US/08265628
'Setent No. 5821094
'Setent No. 5821094
'SENERAL, INFORMATION:
APPLICANT: Rothstein, Steven J.
APPLICANT: GOTHG, Daphne
'ITLE OF INVENTION: S-LOCUS RECEPTOR KINASE GENE IN A
TITLE OF INVENTION: SELF-INCOMPATIBLE BRASSICA NAPUS LINE
```

Gaps

ó

Sequence 2, Application US/09011922A Patent No. 6320022 GENERAL INFORMATION:

RESULT 14 US-09-011-922A-2

g

```
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESS
```

Search completed: October 17, 2002, 14:48:43 Job time: 5.53865 secs

THIS REPORT OF THE PARTY OF THE

١;

```
US-09-070-504-14
                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-070-504-14
                                                                   47
47
47
46.5
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Appli
Appli
Appli
Appli
Appli
Appl
                                                                                                                    October 17, 2002, 14:45:20; Search time 3.49127 Seconds (without alignments) 279.848 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1
Sequence 1
Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                          US-10-018-924-2_COPY_107_146
219
1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
               GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-486-596A-3

US-09-004-713-3

US-09-0070-504-15

US-09-011-922A-3

US-09-011-922A-14

US-09-011-922A-14

US-09-011-922A-14

US-09-011-922A-14

US-09-281-259-4

US-09-281-259-4

US-08-934-222-17

US-08-933-402-17

US-08-532-818-17

US-08-532-818-17
                                                                                                                                                                                                                                                                                                                                                        Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-233-389C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-486-596A-1
                                                                                                                                                                                                                                                                                                                        231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                    - protein search, using sw model
                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               %
Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1000.0
11000.0
11000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database:
                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
```

Sequence

Sequence

```
ö
                          Sequence 2, Ap
Sequence 17, A
Sequence 6, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                        Sequence 15,
                                       sequence 10, sequence 3, sequence 24, sequence 24, sequence 10, sequence 17, sequence 7, sequence 7, sequence 6, sequence 2,
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 52;
                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Smith, Derek D.
APPLICANT: Saha, Shankar
APPLICANT: Abel, Peter W.
TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 219; DB 4; Best Local Similarity 100.0%; Pred. No. 3.6e-26; Matches 40; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
     US-08-265-628-2

US-08-492-459-10

US-08-492-459-10

US-08-495-994-3

US-08-716-873-24

US-09-414-006-10

US-09-167-681-47

US-09-167-681-47

US-09-141-206-6

US-09-141-206-7

US-09-141-206-7

US-09-141-206-7

US-09-141-206-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Mueting, Raasch & Gebhardt, P.A. STREET: 119 No. 6268474th Fourth Street CITY: Minneapolls STATE: MN
                                                                                                                                                                                                                                        US-08-207-904-15
                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/09070504 Patent No. 6268474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NORTH:
APPLICATION NORTH:
CLASSIFICATION S30
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REGISTRATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,596A FILING DATE: UNR 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 SFGCRFGTCTVQKLAHQIYQFTDKDKDKNVAPRSKISPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 219; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 40; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: JUNE 7, 1995
CLASSIFICATION: 530
ATTORNEY/AGBNT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIVI
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08486596A
; Sequence 1, Application US/08486596A
; Patent No. 5837823
; GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenj1
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-486-596A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-801-863-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match

Ouery Match

100.0%; Score 219; DB 1; Length 185;

Best Local Similarity 100.0%; Pred. No. 1.6e-25;

Matches 40; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CIP: 10020
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
OFFRANTOG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATA:
APPLICATION NUMBER: US/08/233,389C
FILNG DATE: 16-APR-1994
ATTORNEY/AGENT INPOMMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
RELECOMMUNICATION INFORMATION:
TELEFARM (212) 566-9000
TELEFARM: (212) 566-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                              APPLICANT: KTAMMRA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08801863
Patent No. 5830703
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KITAMURA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanemao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                        Sequence 1, Application US/08233389C Patent No. 5639855 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-233-389C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10020
                                                                                                         JS-08-233-389C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-801-863-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                  RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

Gaps

ö

Length 185; Indels

```
Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/23,389C
FILING DATE: 26-APR-1994
FILING DATE: 26-APR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr. James F.
REGISTRATION NUMBER: SHGN-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFRONE: (212) 596-9000
TELEFRATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPOTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,863
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 530
ATTONNEY/AGBET INPORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET UNMBER: 27,794
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION 1NFORMATION:
TELEPHONE: (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 213; DB 1; L
Pred. No. 1.3e-24;
0; Mismatches 1;
             1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08801863
Patent No. 5830703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 97.3%;
Best Local Similarity 97.5%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                               New York
                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                              COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-233-389C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-801-863-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                              ö
                                              Gaps
                                            ö
       Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 185;
                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 SFGCRFGTCTVQKLAHQIYQFTDKDKVAPRSKISPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146
100.0%; Score 219; DB 2;
100.0%; Pred. No. 1.6e-25;
tive 0; Mismatches 0;
                                                                        1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 219; DB 2; Best Local Similarity 100.0%; Pred. No. 1.6e-25; Matches 40; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                     Sequence 1, Application US/09004713
Fatent No. 5910416
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08233389C
Patent No. 563985
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KATAMURA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: MATSUO, Hisayuki
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C/O FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
                     Best Local Similarity 100.
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-004-713-1
                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
US-08-233-389C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: N
COUNTRY:
                                                                                                                                                                                   US-09-004-713-1
   Query Match
                                                                                                             д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
```

KANGAWA, Kenji

```
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 188;
                                                                                                                           Length 188;
                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,596A
FILING DATE: JUNE 7, 1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 SFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKISPQGY 146
                                                                                                                                                                                                                      107 SFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKISPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                   1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 213; DB 2;
Pred. No. 1.3e-24;
0; Mismatches 1.
                                                                                                                           Score 213; DB 2;
Pred. No. 1.3e-24;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION UNBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIVI
TELECOMMUNICATION INFORMATION:
TELEPHORE: (212) 596-9000
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08486596A
Patent No. 5837823
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KITAMURA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: PETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1251 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-004-713-3
; Sequence 3, Application US/09004713
Patent No. 5910416
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 97.3%;
Best Local Similarity 97.5%;
Matches 39; Conservative (
                                                                                                                             Query Match 97.3%;
Best Local Similarity 97.5%;
Matches 39; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KITAMURA, Kazuo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
                    188 amino acids
 SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                                                 TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-801-863-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-486-596A-3
                                                                                                                                                                                                                                                                                                               US-08-486-596A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
                                                                                                                                                                                                                                                                                              RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                       à
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: STATEM, Derek D. APPLICANT: STATEM, Derek D. APPLICANT: Sha, Shankar APPLICANT: Sha, Shankar APPLICANT: She, Shankar APPLICANT: Abel, Peter W. TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE NUMBER OF SEQUENCES: 23
ADDRESSEE: Mueting, Raasch & Gebhardt, P.A. STREET: 119 No. 6268474th Fourth Street
CITY: Minneapolis
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN RALEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,504
                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: JANUARY 7, 1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 SFGCRFGTCTVQKLAHQIYQFTDKDKDKDGVAPRSKISPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 213; DB 2;
Pred. No. 1.3e-24;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE, DOCKET NUMBER: SHGN-5 DIV2 CON
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
                                                                                                    ADDRESSEE: C/O FISH & NEAVE STREET: 1251 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMBER: US/09/070,504
30-APR-1998
APPLICANT: MATSUO, HISAYUKI
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: c/o FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-070-504-15

Sequence 15, Application US/09070504

Patent No. 6268474

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.3%;
97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-004-713-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 39; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                  ZIP: 10020
                                                                                                                                                                            N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                COUNTRY:
```

```
Sequence 3. Application US/09011922A

Patent No. 6320022

GENERAL INPORMATION:

APPLICANT: Cuttitta, Frank; Martinez,

APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward

APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward

APPLICANT: As and Ascii, Charles

TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related

TITLE OF INVENTION: Product (PAMP) in Human Pathology and

TITLE OF INVENTION: Physiology

NUMBER OF SEQUENCES: INVENTION: Physiology

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.4%; Score 163; DB 4; L
100.0%; Pred. No. 5.6e-18;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIDM TYPE: FIOPPY DISK
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS WORD 97
SOFWWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,922A
FILING DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/002,514
FILING DATE: 18-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/002,936
FILING DATE: 30-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 12-Mar-1996
PRIOR APPLICATION DATA:
FILING DATE: 12-Mar-1996
PRIOR APPLICATION DATA:
FILING DATE: 16-Aug-1996
FILING DATE: 16-Aug-1996
FILING DATE: 16-Aug-1996
FILING DATE: 16-Aug-1996
APPLICATION NUMBER: PCT/US96/13286
FILING DATE: 16-Aug-1996
APPLICATION NUMBER: PCT/US96/13286
FILING DATE: 16-Aug-1996
APPLICATION NUMBER: PCT/US96/13286
FILING DATE: 16-Aug-1996
ANDERS TOORNEY AND AUGHT OF 
                1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: MORGAN & FINNEGAN, L.L.P.
345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: PreproAM(116-146)
US-09-011-922A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Leslie A. Serunian
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: NY COUNTRY: USA ZIP: 10154-0053 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 31 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                      US-09-011-922A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23, Application US/09070504

Batent No. 6268474

GENERAL INFORMATION:
APPLICANT: Smith, Derek D.
APPLICANT: Saha, Shankar

APPLICANT: Saha, Shankar

APPLICANT: Saha, Shankar

TILLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
TILLE OF INVENTION: SUPERFAMILY AND METHODS OF USE

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
ADDRESSEE: Mucting, Raasch & Gebhardt, P.A.
STREET: Minneapolis

CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 50,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: USAN

ZIP: 5401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,504
FILING DATE: 30-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCCOTMACK, Myra H
REFERENCE/DOCKET NUMBER: 180.00020101
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION ON: 23:
TELEFONE: 612/305-1228
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 74.4%; Score 163; DB 4; I
Best Local Similarity 100.0%; Pred. No. 5.6e-18;
Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 196; DB 4
Pred. No. 1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
NAME: McCormack, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180.00020101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                TELEFAX: 612/305-1228
INPORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS: LENGTH: 50 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 87.5
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                      US-09-070-504-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-070-504-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-070-504-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
```

Gaps

ö

RESULT 13

```
APPLICANT: Cuttitta, Frank; Martinez,
APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
APPLICANT: Karen; Macri, Charles
TTILE OF INVENTION: Functional Role of
TTILE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
TTILE OF INVENTION: Product (PAMP) in Human Pathology and
TTILE OF INVENTION: Physiology
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.0%; Score 57; DB 4; Length 13; 100.0%; Pred. No. 0.02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: YGG-PreproAM (122-131)
US-09-011-922A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/011,922A
FILING DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/002,514
FILING DATE: 18-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/002,936
FILING DATE: 30-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/013,172
FILING DATE: 10-Aug-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/013,172
FILING DATE: 11-Aug-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lealie A. Serunian
RECISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4202US3
TELECOMMUNICATION INFORMATION:
TE
                                                                                                                                                                                                                                                                                                                                 MORGAN & FINNEGAN, L.L.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08966388
Patent No. 5965412
GENERAL INFORMATION:
APPLICANT: Michia KUBOTA
APPLICANT: Michia KUBOTA
APPLICANT: Hiroto CHAEN
APPLICANT: Toshio MIYAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS WORD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                   STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 26.0
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 HQIYQFTDKD 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 HQIYQFTDKD 13
                                                                                                                                                                                                                                                                                                                                                                                                        New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: P071
                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-08-966-388-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                              Sequence 14, Application US/09011922A

Patent No. 6320022

GENERAL INFORMATION:

APPLICANT: Cuttifta, Frank; Martinez,
APPLICANT: Cuttifta, Frank; Martinez,
APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
APPLICANT: Taffedo; Milliam; Walsh, Thomas; Grey,
APPLICANT: Karen; Macri, Charliam; Walsh, Thomas; Grey,
APPLICANT: Karen; Macri, Charliam; Role of
TITLE OF INVENTION: Functional Role
TITLE OF INVENTION: Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic homolog of two-thirds of the intact AM peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.4%; Score 163; DB 4; L
100.0%; Pred. No. 5.6e-18;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Leslie A. Serunian
REGISTRATION NUMBER: 35,353
REERENECAPOCKET NUMBER: 2026-4202US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRICATION NUMBER: US/60/002,514
FILING DATE: 18-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/002,936
FILING DATE: 30-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/013,172
FILING DATE: 12-Mar-1996
PRIOR APPLICATION NUMBER: PCT/US96/13286
FILING DATE: 16-Aug-1996
APTICATION NUMBER: PCT/US96/13286
FILING DATE: 16-Aug-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSER: MORGAN & FINNEGAN, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: MS WORD 97
SOFTWARE: ASCII
CURRENT APPLICATION NUMBER: US/09/011,922A
FILING DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 2, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
COTHER INFORMATION:
US-09-011-922A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-09-011-922A-2
                US-09-011-922A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

Gaps

```
TITLE OF INVENTION: KOJIBIOSE PHOSPHORYLASE, ITS PREPARATION AND USES NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CITY: Washington Street, N.W., Suite 300
COUNTRY: USA
COUNTRY: USA
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent IN PC-DOS/MS-DOS
SOFTWARE: Patent IN Release #1.0, Version #1.30
CURRENT APPLICATION NAMBER: US/08/966,388
FILING DATE: 8-NOV-1996
FILING DATE: 8-NOV-1996
FILING DATE: 3-MAR-1997
ATTONREY/AGENT INFORMATION:
NAME: BROWNY, ROGET L.
REGISTRATION NUMBER: 25,618
FELECOMMUNICATION NUMBER: 25,618
FERERENCE/DOCKET NUMBER:
TELECOMMUNICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.7%; Score 52; DB 2; Length 775; 36.0%; Pred. No. 15; tive 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 248633

INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTENISTICS:..
LENGTH: 775 amino acids
TYPE: amino acid
TYPE: amino acid
MOLECULE TYPE: peptide
US-08-966-388-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 36.05
Matches 9; Conservative
```

Search completed: October 17, 2002, 14:48:42 Job time: 5.49127 secs

ò qq

ö

Gaps

THIS PAGE BLANK (USPTO)

ļ

Ġ

```
October 17, 2002, 14:45:20 ; Search time 12.5786 Seconds (without alignments) 459.181 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results, predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A_Geneseq_032802:*

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseqy-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseqy-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseqy-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseqy-embl/AA1999.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                US-10-018-924-2_COPY_95_146
283
1 YRQSMNNFQGLRSFGCRFGT......FTDKDKDNVAPRSKISPQGY
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΙD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
```

	12	283	0	185	22	AAB60344	Human adrenomedull
	13 14	277 277	م م	188 188	22	AAB49698 AAB60345	Porcine adrenomedu Porcine adrenomedu
	15 16	231	ب ب	185	22	AAE09819 AAB49699	Rat adrenomedullin
	17	231	90	185	222	AAB60346 AAB91765	Rat adrenomedullin
	19 20	219.5 196	77.6	53	22	AAB91767 AAB91768	Adrenomedullin pep
		181.5 163	1,9	37	22 18	AAB91761 AAW25160	Adrenomedullin pep Human preproadreno
	23	163 163	ب ب	31	22	AAB91762 AAE09827	Adrenomedullin pep
	25	64		1547	22	AAB91760	Adrenomedullin pep
	27	09	9 79	231	21	AAB11449	Kac Canalicular mu Human CMOAT C-term
	28 20	00	4,0	231	21	AAB28224	
	30	23	100	1545	16	AAW55966	Human canalicular
	31 32	56.5	н с	1346	18	AAW25159 ARR65953	Human preproadreno
	33	26	00	339	21	AAB26100	Mycobacterium auru
	3.5	2 0	ω œ	333	21	AAB26104 ARB67015	Mycobacterium auru Drosophila melanog
	36	26	000	828	12	AAR53404	S-Locus receptor (
	37	26	<u>م</u> د	858	19	AAW49080	Brassica sp. S-rec
	3 G	22	χ <del>4</del>	292	27	ABB65954 AAY75592	Drosophila melanog Neisseria gonorrhe
	40	55	4	1344	22	ABB59224	
	41	54.5	m c	482	21	AAG14118	Arabidopsis thalia
	4 4	54.5	u w	482	77	AAG54151 AAG14117	Arabidopsis thalia Arabidopsis thalia
	44	54.5	m c	483	21	AAG54150	Arabidopsis thalia
	<b>4</b> 0	04.0	າ.	φ Ο ν	77	AAG54149	Arabidopsis thalia
						ALIGNMENTS	
RESULT AAB7511	7LT 1						
Q;	AAB75110		standard;	Protein	n; 5	2 AA.	
¥C Y	AAB7	5110;					
×	,		1 6 5 4 4				
XX	JL-16	JUL-2001	(Ilrst	entry	<u>.</u>		
DE	Нишап		adrenomedulli	in (AM)		protein.	
XX	200	1.10000			1		
X X X	adre	Adrenomedullin adrenomedullin	• •	giycine e precursor;	×		adrenomedullin; AM; AM-gly; protein; pharmaceutical; diagnostic.
so	Ношо	sapiens					
XX	W0200	WO200127310	- 141				
XX	19-ADP	PP-2001					
×	١	1	•				
PF	10-0CT	-2000	. 5	000WO-JP0702	23.		
PR	15-0CT	TT-1999	; 99JP	-029414	47.		
XX PA	(SHIO	_	SHIONOGI &	со гтр			
Id	Takimoto	noto A,	Mitsud	a Y,	Nakay	yama T, Mitsushima	na K;
X K K	WPI; N-PSL	WPI; 2001-28 N-PSDB; AAH	01-282044/29 AAH19806.				
V L	Produ	icing a	adrenomedullin	ullin	nsefnl	for	and diagnost
PT	appli recom	application recombinant	comprises host -		producing	fuse	in precursor u
	) ) )		)				

×

Human adrenomeduli

Glycine extended h Glycine extended a Linker peptide-adr UspA(1-57)-(A)-(GS UspA(1-84)-(A)-(GS UspA(1-84)-(A)-(GS Thioredoxin-(GSGSG

AAB75111 AAB75113 AAB75122 AAB75123 AAB75123 AAB75124 AAB75124 AAB75114

52 52 53 53 53 62 120 1170 1170

1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0

283 283 283 283 283 283 283 283

10 10 10 11 11

Adrenomedullin pep Human adrenomedull Human adrenomedull

AAB75110 AAB91759 AAE09818

```
Saha S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-564216/63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                              Human; vasoactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 AA;
                                                                                     52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                           US6268474-B1
                                                                                                                                                                                                                                                                                                           29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Simi
Matches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                  AAE09818;
                                                                                       Sequence
                                                                                                               Query Match
                                                                                                                                           Matches
                                                                                                                                                                                                                                             AAE0981
                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                          g
8888888888888
                                                                                                                                                                  ð
                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidy) and malenimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptides stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various discorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.
                                  adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           Protection, endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                 52
                                                                                                                                                                               100.0%; Score 283; DB 22; Length 52; 100.0%; Pred. No. 2.6e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thibaudeau K;
                         invention describes a method (M1) for producing
                                                                                                                                                                                                                                               1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                         Indels
                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DI,
                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Holmes
                                                                                                                                                                                                                                                                                                                                                                                                   Adrenomedullin peptide (AM) SEQ ID NO:935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 498; 733pp; English.
 Disclosure; Page 45; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Milner PG,
                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                        AAB91759 standard; Peptide; 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0134406.
99US-0153406.
99US-0159783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAY-2000; 2000WO-US13576
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-112059/12.
                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                      52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200069900-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens
                                                                                                                                                                                                                                                                                                                                                                          22-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-NOV-2000
                                                                                                                                                                                                         52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bridon DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                  AAB91759
                                                                                                                                                       Sequence
                                                                                                                                                                               Query Match
                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo
                                                                                                                                                                                                                                                                                                           AAB91759
                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                          셤
 & X C C C C C C C C X X X
```

```
ö
                                                                                                                                                                                                                                                                                                                              ö
Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to antagonists of the vasoactive peptide calcitonin gene related peptide (CGRP) and other members of the CGRP superfamily. The invention also relates to amino the terminal modifications of peptides to improve their ability to bind to a member of the CGRP-receptor super-family. CGRP antagonists are used for inhibiting CGRP activity which can be used in vitro e.g. in assays to identify and/or isolate CGRP receptors or with intact cells either in vitro or in vivo to inhibit the effect of CGRP binding to its receptor. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vasoactive peptides useful for inhibiting calcitonin gene related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide; calcitonin gene related peptide; CGRP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52
                                                                                                                                                                                                                                                                                                                                                                                        52
                                                                                                                                                                                                                                                                                                                                                                                                                                            52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 52;
                                                                                                                                                                                                                                                                      52;
                                                                                                                                                                                                                                                                                                                                                                                                                            1 YROSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                           1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 283; DB 22;
Llarity 100.0%; Pred. No. 2.6e-32;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                      100.0%; Score 283; DB 22; 100.0%; Pred. No. 2.6e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGRP-receptor identification; adrenomedullin.
                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Column 25-26; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human adrenomedullin peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE09818 standard; peptide; 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Abel PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0070504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide receptor activity
                                                                                                                                                                                                                                                                                                                                    52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYCR-) UNIV CREIGHTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adrenomedullin peptide
```

4

```
10-OCT-2000; 2000WO-JP07023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAH19809
       WO200127310-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-APR-2001
                                                                                                               rakimoto A,
                             19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB75113;
                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB75113
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                        adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                 Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host \dot{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                               Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 283; DB 22; Length 53; 100.0%; Pred. No. 2.7e-32; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a method (M1) for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YROSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                           Glycine extended human adrenomedullin (AM-gly) protein.
                                                                                                                                                                                                                                                                             Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycine extended adrenomedullin (AM-gly) protein.
                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 46; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA.
                             AAB75111 standard; Protein; 53 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB75112 standard; Protein; 53
                                                                                                                                                                                                             10-OCT-2000; 2000WO-JP07023
                                                                                                                                                                                                                                   99JP-0294147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                       (first entry)
                                                                                                                                                                                                                                                         (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
nes 52; Conservative
                                                                                                                                                                                                                                                                                                WPI; 2001-282044/29.
N-PSDB; AAH19807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 AA;
                                                                                                                                                                    WO200127310-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                   15-0CT-1999;
                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JUL-2001
                                                                       31-JUL-2001
                                                                                                                                                                                         19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB75112;
                                                 AAB75111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB75112
        RESULT 4
                    AAB7511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a method (M1) for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Linker peptide-adrenomedullin (AM) precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitsushima K;
                                                                                                        Nakayama T, Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 283; DB 22;
100.0%; Pred. No. 2.7e-32;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakayama T,
                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 47; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB75113 standard; Protein; 62 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-OCT-2000; 2000WO-JP07023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99JP-0294147
99JP-0294147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                     (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pakimoto A, Mitsuda Y,
                                                                                                        Mitsuda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SHIO ) SHIONOGI & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-282044/29.
                                                                                                                                                          2001-282044/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 AA;
                                                                                                                                                             WPI; 2001-282044,
N-PSDB; AAH19808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200127310-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-OCT-1999;
15-OCT-1999;
```

exemplification of the present invention.

120 AA;

Sequence

SXS

```
RESULT 9
AAB75124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                               adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAMI19806 to AAM19866 and AAB75110 to AAB75124 repersent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method (MI) for producing adrenomedulin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19806 and AAB75124 represent sequences which are used in the
                             Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; glycine extended adrenomedullin; AM; AM-gly; precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 62;
                                                                                                                                                                                                                 The present invention describes a method (M1) for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 283; DB 22; 100.0%; Pred. No. 3.3e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takimoto A, Mitsuda Y, Nakayama T, Mitsushima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UspA(1-57)-(A)-(GSGSGDAFE)-AM-gly protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB75122 standard; Protein; 120 AA.
                                                                                                                                                      Page 48; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Page 68; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99JP-0294147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-OCT-2000; 2000WO-JP07023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-282044/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 AA;
                                                                                           recombinant host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAH19864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adrenomedullin;
adrenomedullin p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200127310-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-APR-2001
                                                                                                                                                          Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB75122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A PART OF THE PART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

6

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method (M1) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host -
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
      Length 120;
                                                                                                                                                         68 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119
                                                                                                                                  52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 120;
                                                                                                                     1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitsushima K;
   Score 283; DB 22;
Pred. No. 7.1e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 283; DB 22;
100.0%; Pred. No. 7.1e-32;
live 0; Mismatches 0;
                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UspA(1-56)-(DD)-(GSGSGDAFE)-AM-gly protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; Page 69-70; 75pp; Japanese
                                                                                                                                                                                                                                                                                                                                                   Ź
                                                                                                                                                                                                                                                                                                                                            AAB75123 standard; Protein; 120
                                                                 ;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2000; 2000WO-JP07023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99JP-0294147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SHIO ) SHIONOGI & CO LTD.
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takimoto A, Mitsuda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-282044/29
Query Match
Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAH19865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200127310-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                          AAB75123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                   NAMES OF COLOR OF STREET O
                                                                                                                           ò
                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
```

```
The present invention describes a method (MI) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AMH19806 to AMH19806 and AAB7510 to AAB75124 repersent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                          rrouwing agrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for promoting passive elongation of vesicle smooth muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Passive elongation; vesicle smooth muscle; uropathic activity; adrenomedulin; urinary disorder; incontinence; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 283; DB 22;
Pred. No. 1.1e-31;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human adrenomedulin amino acid sequence.
                                                                                                                                                   Nakayama T,
                                                                                                                                                                                                                                                                                                               Claim 17; Page 49-50; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ŗ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB49697 standard; Protein; 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99JP-0177549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JUN-2000; 2000WO-JP04166
                                                10-OCT-2000; 2000WO-JP07023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHIO ) SHIONOGI & CO LTD
                                                                                                                (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprises adrenomedulin
                                                                                                                                                     Mitsuda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-080754/09.
N-PSDB; AAF29138.
                                                                                                                                                                                       WPI; 2001-282044/29.
N-PSDB; AAH19810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200078338-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition
                                                                               15-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-DEC-2000
                                                                                                                                                     Takimoto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yanagita T;
           19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB49697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB49697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a method (M1) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications, AAH19806 to AAH19866 and AAB75110 to AAB75124 repersent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ಥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using recombinant host.
                                                                                                                                      Adrenomedullin, glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitsushima
                                                                                                       JspA(1-84)-(A)-(GSGSGDAFE)-AM-gly protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thioredoxin-(GSGSGDAFE)-AM-gly protein
                                                                                                                                                                                                                                                                                                                                                                                                                          Nakayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB75114 standard; Protein; 170 AA.
 ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 17; Page 71; 75pp; Japanese.
 AAB75124 standard; Protein; 147
                                                                                                                                                                                                                                                                                                                    10-OCT-2000; 2000WO-JP07023.
                                                                                                                                                                                                                                                                                                                                                       99JP-0294147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         (SHIO ) SHIONOGI & CO LTD.
                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            rakimoto A, Mitsuda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-282044/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAH19866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200127310-A1
                                                                                                                                                                                                                                                WO200127310-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
                                                                                                                                                                                            Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                       15-OCT-1999;
                                                                    31-JUL-2001
                                                                                                                                                                                                                                                                                   19-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                 AAB75124:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
AAB75114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
```

g ö

ö

Gaps

;

Indels

52

Length 170;

producing the fused

Mitsushima K;

ö

Gaps

; 0

; 0

146

52

uropathic activity;

```
This invention relates to a composition for promoting passive elongation of vesicle smooth muscle. The composition contains adrenomedulin, and has uropathic activity. The composition can be used for promoting passive elongation of vesicle smooth muscles, this is useful for releving uninary disorders such as impending urinary incontinence, reflex urinary incontinence and urinary incontinence with overflow. The present sequence composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition for promoting passive elongation of vesicle smooth muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Porcine; pig; adrenomedullin; precursor; bradykinin antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                 vesicle smooth muscle; uropathic acary disorder; incontinence; procine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 277; DB 22;
Pred. No. 8.4e-31;
0; Mismatches 1;
     Mismatches
                                                                                                                                                                                                                                                                            Porcine adrenomedulin amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 31-33; 42pp; Japanese.
                                                                                                                                                                  AAB49698 standard; Protein; 188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porcine adrenomedullin precursor.
     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB60345 standard; Protein; 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.9%;
98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUN-2000; 2000WO-JP04166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99JP-0177549
                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 98.1
Matches 51, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprises adrenomedulin
                                                                                                                                                                                                                                                                                                                                  adrenomedulin; urinary
                                                                                                                                                                                                                                                                                                                   Passive elongation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-080754/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAF29139
                                                                                                                                                                                                                                                                                                                                                                                                          WO200078338-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUN-1999;
                                                                                                                                                                                                                                           04-APR-2001
52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                              28-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yanagita T;
                                                                                                                                                                                                      AAB49698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB60345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
 Matches
                                                                                                                               RESULT 13
                                                                                                                                                AAB49698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                       g
                                      à
                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XXEX DXXXX
                                                                                                                                                                                                                                                                                           ô
                                          This invention relates to a composition for promoting passive elongation of vesticle smooth muscle. The composition contains adrenomedulin, and has uropathic activity. The composition can be used for promoting passive elongation of vesticle smooth muscles, this is useful for relieving unitary disorders such as impending urinary incontinence, reflex urinary incontinence and urinary incontinence with overflow. The present sequence composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a composition containing adrenomedullin for inhibiting automatic uterine contraction or contraction caused by bradykinin. The invention also relates to the use of adrenomedullin in the preparation of a drug for preventing premature birth or miscarriage. The composition of the invention can be used for preventing premature birth, preventing miscarriage, stopping delivery before caesarean section or for treating dysmenorrhoea. The present sequence represents human adrenomedullin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition for inhibiting automatic uterine contraction or contraction caused by bradykinin comprises adrenomedullin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; adrenomedullin; precursor; bradykinin antagonist;
uterine contraction inhibitor; premature birth; miscarriage; abortion;
dysmenorrhoea; obstetric; gynaecological.
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                            Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 185;
                                                                                                                                                                                                                                                                                                                      1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                               100.0%; Score 283; DB 22;
100.0%; Pred. No. 1.2e-31;
ilve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 283; DB 22;
Pred. No. 1.2e-31;
     Claim 1; Page 26-27; 42pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 37-38; 54pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB60344 standard; Protein; 185 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human adrenomedullin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2000; 2000JP-0079171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUN-2000; 2000WO-JP04167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99JP-0177548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-080755/09.
                                                                                                                                                                                                          185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAF27228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200078339-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tanagita T;
                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB60344;
                                                                                                                                                                                                                                                 Query Match
```

RESULT 12 AAB60344

à g ő

Gaps

ö

Indels

Length 188;

22

Sequence Query Match Best Local

```
calcitonin gene related peptide (CGRP) and other members of the CGRP superfamily. The invention also relates to amino the terminal modifications of peptides to improve their ability to bind to a member of the CGRP-receptor super-family. CGRP antagonists are used for inhibiting CGRP activity which can be used in vitro e.g. in assays to identify and/or isolate CGRP receptors or with intact cells either in vitro or in vivo to inhibit the effect of CGRP binding to its receptor. The present sequence is rat adrenomedullin peptide.
                  Vascactive peptides useful for inhibiting calcitonin gene related peptide receptor activity \boldsymbol{\cdot}
                                                                                        The invention relates to antagonists of the vasoactive peptide
                                                                                                                                                                                                                                                                                                                 Score 231; DB 22;
Pred. No. 5.1e-25;
3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                   Search completed: October 17, 2002, 14:47:59 Job time : 12.5786 secs
                                                               English.
                                                                                                                                                                                                                                                                 81.6%;
84.6%;
                                                               Claim 5; Column 25-26; 24pp;
                                                                                                                                                                                                                                                                                             44; Conservative
WPI; 2001-564216/63
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                        50 AA;
                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                 g
  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                              The invention relates to a composition containing adrenomedullin for inhibiting automatic uterine contraction or contraction caused by bradykinin. The invention also relates to the use of adrenomedullin in the preparation of a drug for preventing premature birth or miscarriage. The composition of the invention can be used for preventing premature birth, preventing miscarriage, stopping delivery before caesarean section or for treating dysmenorrhoea. The present sequence represents porcine adrenomedullin precursor.
                                                                                                                                                                                                                                                                                  Composition for inhibiting automatic uterine contraction or contraction
 uterine contraction inhibitor; premature birth; miscarriage; abortion; dysmenorrhoea; obstetric; gynaecological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat; vasoactive peptide; calcitonin gene related peptide; CGRP; CGRP-receptor identification; adrenomedullin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 277; DB 22; Length in Pred. No. 8.4e-31;
                                                                                                                                                                                                                                                                                               caused by bradykinin comprises adrenomedullin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                           Disclosure; Page 43-44; 54pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.9%;
98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0070504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0070504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE09819 standard; peptide;
                                                                                                                                                              21-MAR-2000; 2000JP-0079171
                                                                                                                        23-JUN-2000; 2000WO-JP04167
                                                                                                                                                 99JP-0177548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat adrenomedullin peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                          CHIO 9, ISONOIHS ( OIHS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saha S, Abel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CREIGHTON
                                                                                                                                                                                                                                            WPI; 2001-080755/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 AA;
                                                                                                                                                                                                                                                          N-PSDB; AAF27229
                                                                    W0200078339-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYCR-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6268474-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-APR-1998;
                                                                                                                                                   23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JUL-2001
                                                                                               28-DEC-2000
                                                                                                                                                                                                                   Yanagita T;
                                            Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE09819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE09819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
```

1;

Gaps

5

3,

Length 50; Indels THIS PAGE BLANK (WATO)

-

```
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

October 17, 2002, 14:45:20; Search time 5.96509 Seconds (without alignments) 837.648 Million cell updates/sec Run on:

Perfect score:

US-10-018-924-2\_COPY\_95\_146 283 1 YRQSMNNFQGLRSFGCRFGT......FTDKDKDNVAPRSKISPQGY Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	adrenomedullin pre	adrenomedullin - p	adrenomedullin pre	monophenol monooxy	S-locus-specific q	canalicular multid	conserved hypothet	multidrug resistan	hypothetical prote		•=	S-receptor kinase	ABC transporter AT	monophenol monooxy	S-locus-specific g	S-receptor kinase	lipopolysaccharide	hypothetical prote		24	hypothetical prote		S-locus-specific g	S-locus-specific q	pectate lyase-like	hypothetical prote	S-locus-specific g	yogenesi	probable ABC trans
	ΙD	JN0684	S41600	JN0766	JC1392	T14536	S71839	н81690	S71841	A99638	A85489	T14415	T07809	AG2058	PC4153	T14529	JQ1677	G84107	T15540	820799	E69130	E91004	E85637	T07814	A27827	T46165	T05598	T14533	œ	H95398
	DB	5	7	7				7				7	7	2	7	7		7					7	7	~	7	7	7	7	~
	Length	185	188	185	532	430	1541	253	1545	189	189	431	429	712	273	428	828	373	465	319	444	93	93	428	436	463	370	429	107	358
d₽	Query Match	100.0	97.9	81.6		21.7	21.6	21.4	20.8	20.7	20.7	20.7	20.3	20.3	20.1	9.	19.8	9	σ	19.4	19.4	19.3	19.3		19.3	19.3	19.1		18.9	18.9
	Score	283	277	231	65.5	61.5	61	60.5	29	58.5	58.5	58.5	57.5	57.5	57	26		55.5	വ	55	55	54.5	54.5	54.5	54.5	54.5	54	54	53.5	53.5
	Result No.	-	7	m	4	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote S-locus-specific g	5-Iocus-specific g hypothetical prote virulence-associat	protein T12C24.12 monophenol monooxy	protein kinase C ( protein kinase C ( protein kinase C (	protein kinase C ( protein kinase C (	hypothetical prote S-locus-specific g S-locus-specific g
B83963 T14424	T14423 T23197 C82867	G86259 YRHU1	KIRTC KIMSCA	KIRBC KIBOC	T21052 T14416 T14530
000	7 77 7	7 - 7			1000
362	428 617 151	522	672 672 672	672 672 675	2374 428 428
18.9	18.9	18.7	18.7 18.7	18.7	18.7 18.6 18.6
53.5	53.5 53	ທີ່ຕຸດ	533	ນຕາ	53 52.5 52.5
30	3 3 3 4 8 9 8	36	38 39	4 4 4 0 1 4	4 4 4 4 4 4 0

## ALIGNMENTS

RESULT 1

_	100000
	1 NOON 1
	adrenomedulin precursor - numan
	C;Species: Homo sapiens (man)
-	C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
	C; Accession: JC2351; JN0684; PN0548; JN0476
	R;Ishimitsu, T.; Kojima, M.; Kanqawa, K.; Hino, J.; Matsuoka, H.; Kitamura, K.; Eto,
	Biochem. Biophys. Res. Commun. 203, 631-639, 1994
	A; Title: Genomic structure of human adrenomedullin gene.
	A;Reference number: JC2351; MUID:94354869
	A; Accession: JC2351
	A; Molecule type: DNA
	A; Residues: 1-185 <ish></ish>
	A;Cross-references: GB:S73906; NID:9765329; PIDN:AAC60642.1; PID:9765330
	A; Experimental source: pheochromocytoma
	R;Kitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.
-	Biochem. Biophys. Res. Commun. 194, 720-725, 1993
	A; Title: Cloning and characterization of cDNA encoding a precursor for human adrenome
	A; Reference number: JN0684; MUID: 93343928
	A; Accession: JN0b84
_	. A; Molecule type: mRNA
_	A; Residues: 1-185 <kit></kit>
	A;Cross-references: GB:D14874; NID:g455470; PIDN:BAA03589.1; PID:g500612
	A; Accession: PN0548
	A; Molecule type: protein
	A; Residues: 22-41 <ki2></ki2>
	R:Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto,
_	Biochem. Biophys. Res. Commun. 192, 553-560, 1993
_	A; Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocy
_	A:Reference number: JN0476; MUID:93249425
_	A: Accession: JN0476
	A; Molecule type: protein
	A; Residues: 95-146 <ki3></ki3>
	A; Experimental source: pheochromocytoma
	C;Genetics:
	A;Gene: GDB:ADM
_	A;Cross-references: GDB:217070; OMIM:103275
	A;Map position: 11pter-11qter
	A;Introns: 33/2; 83/2
	C; Keywords: amidated carboxyl end; blood pressure control; hormone
	F;1-21/Domain: signal sequence #status predicted <sig></sig>
	F;22-185/Product: proadrenomedullin #status predicted <peu></peu>
	F:22-41/Domain: proadrenomedullin amino-terminal 20 peptide *status predicted <pap></pap>
	F;95-146/Product: adrenomedullin #status experimental AMAIN
	F:14/-1857-Domain: carboxyr-terminal propeptice #status predicted curry. F:17-4/-1857-Domain: carboxyr-terminal propeptice #status predicted curry.
	Fill-115/Misulfide bonds: #status experimental
	F:146/Wolfied site: amidated carboxyl form (Tvr) (amide in mature form from following
-	

ö

Gaps ; 0

Query Match
100.0%; Score 283; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 4.7e-30;
Matches 52; Conservative 0; Mismatches 0; Indels

-

ö g

```
R;Takase, M.; Miura, I.; Nakata, A.; Takeuchi, T.; Nishioka, M.

Ggene 121, 359-363, 1992

Gene 121, 359-363, 1992

A;Title: Cloning and sequencing of the CDNA encoding tyrosinase of Japanese pond frog A;Reference number: JC1392, MUID:93077054

A;Recession: JC1392

A;Rocession: JC132

A;Rocession: JC32 <TAKA

A;Residues: 1-532 <TAKA

A;Residues: DBJ:D12514; NID:9222946; PIDN:BAA02077.1; PID:9222947

R;Miura, I.; Okumoto, H.; Makino, K.; Nakata, A.; Nishioka, M.
Jpn. J. Genet. 70, 79-92, 1995

A;Title: Analysis of the tyrosinase gene of the Japanese pond frog, Rana nigromaculat
A;Reference number: I51169; MUID:95290234

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-9, A', 11-277 <MUU>
A;Residues: 1-9, A', 11-277 <MUU>
A;Residues: 1-9, A', 11-277 <MUU>
A;Cross-references: GB:D37779; NID:9809507; PIDN:BAA07034.1; PID:9809508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: monophenol monooxygenase
C;Reywords: glycoprotein; oxidoreductase; transmembrane protein
F;47,90,115,165,234,294,341,360,375/Binding site: carbohydrate (Asn) (covalent) #stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S-locus-specific glycoprotein - wild cabbage (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C;Accession: T14536
R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Tille: Striking sequence similarity in inter- and intra-specific comparisons of clechanism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A: Reference number: 218078; MUID: 97352858
A; Accession: T14536
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-430 < KUS>
A; Cross-references: EMBL: DB8212; NID: 92351155; PIDN: BAA21946.1; PID: 92351156
C; Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C; Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canalicular multidrug resistance protein - rat
Cispecies: Ratus norvegicus (Norway rat)
Cispecies: Ratus norvegicus (Norway rat)
Cispecies: 10-569-1999 #sequence_revision 10-5ep-1999 #text_change 19-Jan-2001
Cispecies: 10-569-1999 #sequence_revision 10-5ep-1999 #text_change 19-Jan-2001
Cispecies: 151839
Ribuechler, M.; Koenig, J.; Brom, M.; Kartenbeck, J.; Spring, H.; Horie, T.; J.; Bloom, M.; Kartenbeck, J.; Spring, H.; Horie, T.; A; Title: CDNA cloning of the hepatoccyte canalicular isoform of the multidrug A; Reference number: S71839; MuID:96279006
A; Reference number: S71839; MuID:96279006
A; Status: preliminary; nucleic acid sequence not shown
A; Status: preliminary; nucleic acid sequence not shown
A; Residues: 1-1541 <BUE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 QSMNNFQGLRSFGCRFG----TCTVQK--LAHQIYQFTDKDKD-----NVAPRSKISP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCRF-GTCTVQKLAHQIYQFTDKDKD------NVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 23.1%; Score 65.5; DB 2; Best Local Similarity 33.9%; Pred. No. 1.2; Matches 20; Conservative 8; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.7%; Score 61.5; DB 2; 28.6%; Pred. No. 3.2; 11ve 12; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Simi
Matches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A. Accession: PN0610
A. Molecule type: protein
A. Molecule type: prodresor contains a unique 20-amino acid sequence designated proadrenome
C. Comment: This precursor contains a predicted <SIG>
C. Reyworks: amidated carboxyl end
F. 1-2.1/Domain: signal sequence #status predicted <PEU>
F. 22-118/Product: proadrenomedullin #status predicted <PEU>
F. 24.1/Product: proadrenomedullin #status predicted <MAT>
F. 34.1/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gly F: 143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change ll-Jul-1997
C;Accession: JN0766; PN0610
R;Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T Richam Rabopha; Res. Commun. 195, 931-927, 1993
A;Title: Molecular cloning and biological activities of rat adrenomedullin, a hypotensiv A;Reference number: JN0766; MUID:93384621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA
                                                                                                                                                                                                                                                              adrenomedullin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C;Accession: $41600
R;Kitamura, K.; Kangawa, K.; Kojima, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
FEBS Lett. 338, 306-310, 1994
A;Title: Complete amino acid sequence of porcine adrenomedullin and cloning of A;Reference number: $41600; MUID:94139945
A;Steference number: $41600; MUID:94139945
A;Steference number: $41600; MUID:94139945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       monophenol monooxygenase (EC 1.14.18.1) - Japanese pond frog
N;Alternate names: tyrosinase
C;Species: Rana nigromaculata (Japanese pond frog)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C;Accession: JC1392; ISI169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule, type: mRNA
A; Residues: 1-188 <KIT>
A; Cross-references: GB:D14875; NID:g439721; PIDN:BAA03590.1; PID:g496379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                     25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 185;
                                        YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 231; DB 2;
Pred. No. 3.8e-23;
3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 277; DB 2;
Pred. No. 3e-29;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 81.6%;
1 Similarity 84.6%;
44; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.9%;
ilarity 98.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adrenomedullin precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: JN0766
A; Molecule type: mRNA
A; Residues: 1-185 <SAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
```

g à

4

resistan

ä

Gaps

11;

Matches

a ð

```
A; Accession: S.Lusta.
A; Moolecule type: mRNA
A; Residues: 1-1545 < KOE>
A; Cocasion: 1-1545 < KOE>
A; Cocasion: 1-1545 < KOE>
A; Cocas references: EMBL: X96395; NID:g1507819; PIDN:CAA65259.1; PID:g1514568
A; Crocas references: EMBL: X96395; NID:g1507819; PIDN:CAA65259.1; PID:g1514568
B; Buechler, M.; Koenig, J.; Brom, M.; Kartenbeck, J.; Spring, H.; Horie, T.; Keppler, J. Biol. Chem. 271, 15091-15096, 1996
A; Title: cDNA cloning of the hepatocyte canalicular isoform of the multidrug resistan A; Reference number: $71839; MUD:96279006
A; Reference number: $71839; MUD:96279006
A; Reterence number: $71839; MUD:96279006
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1415-1429, VPV', 1432-1455, E', 1457-1545 < RUE>
C; Genetics:
A; Gene: GDB:ABCC2; CNOAT; ABC; MRP2; CNNRP; DJS
A; Cross-references: GDB:6089489; OMIM:601107
A; Map position: 10q24-10q24
C; Superfamily: human multidrug resistance protein cNOAT2; ATP-binding cassette homology cABC1>
C; Keywords: ATP; glycoprotein; nucleotide binding motif A (P-loop)
F; 571-678/Region: nucleotide-binding motif A (P-loop)
F; 1334-1341/Region: nucleotide-binding motif A (P-loop)
F; 1334-1341/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.7%;
ilarity 34.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X96393; NID:g1292881; PIDN:CAA65257.1; PID:g1617207
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology
C;Keywords: ATP; glycoprotein: nucleotide binding; P-loop; transmembrane protein
F;100-124/Domain: transmembrane #status predicted <TMO1>
F;107-151/Domain: transmembrane #status predicted <TMO3>
F;305-329/Domain: transmembrane #status predicted <TMO5>
F;314-311/Domain: transmembrane #status predicted <TMO6>
F;354-381/Domain: transmembrane #status predicted <TMO6>
F;540/Domain: transmembrane #status predicted <TMO9>
F;540/Domain: transmembrane #status predicted <TMO9>
F;550-504/Domain: transmembrane #status predicted <TMO9>
F;650-0833/Domain: transmembrane #status predicted <TMO9>
F;650-0833/Domain: transmembrane #status predicted <TMO9>
F;650-0833/Domain: transmembrane #status predicted <TMO9>
F;650-084/Domain: transmembrane #status predicted <TMO9>
F;650-081/Domain: transmembrane #status predicted <TMO9>
F;650-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;1203-1228/Domain: transmembrane #status predicted <TM13>
F;1313-1506/Domain: ATP-binding cassette homology <ABC2>
F;1330-1337/Region: nucleotide-binding motif A (P-loop)
F;6,1007,1010,1011/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              multidrug resistance protein, canalicular - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 571841, 571840
St;Koenig, J.; Keppler, D.
submitted to the EMBL Data Library, August 1996
A;Reference number: S71841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YRQSMNNF-----QG--LRSFGCR-----FGTCTVQKLAHQIYQFTDKDKDNVA-PRS 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 61; DB 1; Length 1541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;1018-1046/Domain: transmembrane #status predicted <TM11>F;1104-1132/Domain: transmembrane #status predicted <TM12>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 1479 FSQCTVITIAHRLHTIMDSDKIMVLDNGKIVEYG 1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 60.5; DE
Pred. No. 2.5;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 FGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            th 21.4%; Similarity 32.8%; 22; Conservative 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 38.2
nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246 KEAQQDF 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 KISPQGY 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: TC0556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H81690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S71841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
hypothetical protein ECs0073 [imported] - Escherichia coli (strain 0157:H7, substrain C; Species: Escherichia coli C; Species: Escherichia coli C; Species: Bs-dul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C; Accession: A99658 R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and g A; Reference number: A99629; MUID:21156231; PMID:11258796 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-189 < AXX-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein 20078 [imported] - Escherichia coli (strain O157:H7, substrain E C;Species: Escherichia coli C;Decies: Escherichia coli C;Dete: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Decession: A88489 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May liller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
                                                                           ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:BA000007; PIDN:BAB33496.1; PID:g13359529; GSPDB:GN00154 A;Experimental source: strain 0157:H7, substrain RIMD 0509952 C;Genetics:
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ر
ا
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 189;
Query Match 20.8%; Score 59; DB 1; Length 1545; Best Local Similarity 37.8%; Pred. No. 26; Matches 14; Conservative 5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
                                                                                                                                                                                       1483 FAHCTVITIAHRLHTIMDSDKVMVLDNGKIIECGSPE 1519
                                                                                                                                        18 FGTCTVQKLAHQIYQFTDKDKDNVAPRSKI----SPQ 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 58.5; D. Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || |::|: ||:|:|
95 KLTHWLIKFNELKEYAKDPENMAAKASLSPEG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: ECs0073
C;Superfamily: Escherichia coli yabP protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 KLAHQIYQFTD----KDKDNVAPRSKISPQG
```

Thu Oct 17 15:36:27 2002

.,

17; Gaps

Indels

15;

```
ABC transporter ATP-binding protein all2021 [imported] - Anabaena sp. (strain PCC 712 C; Species: Anabaena sp. A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002 C; Accession: AG2058

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:BA000019; PIDN:BAB73720.1; PID:g17131112; GSPDB:GN00179 A;Experimental source: strain PCC 7120 C;Genetics:
                                                                                      209 GLRSHRSGPWNGIRFSGIPEDQXSSYWVYSFTENSEEVAYTFRMTNSSIYSRLKISSEGF 268
                                                        GLRSF-----GCRF-GTCTVQKLAHQIYQFTDKDKD------NVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 QGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monophenol monooxygenase (EC 1.14.18.1) - chicken
        10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 20.3%; Score 57.5;
1 Similarity 37.2%; Pred. No. 18;
16; Conservative 6; Mismatches
        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 35.9 Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-712 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Accession: AG2058
A, Status: preliminary
A, Molecule type: DNA
        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: all2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                           10
        Matches
                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14
                                                           à
                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                A Status: preliminary
*Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-189 <STO>
A; Cross-references: GB:AE005174; NID:g12512769; PIDN:AAG54373.1; GSPDB:GN00145; UWGP:200
A; Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons of class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: SLG(S1)
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: ATP; glycoprotein; magnesium; phosphotransferase; serine/threonine-specific
F;32-427/Domain: S-locus-specific glycoprotein homology <SSG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-receptor kinase (EC 2.7.1.-) - radish (fragment)
NiAlternate names: S glycoprotein
NiAlternate names: S glycoprotein
C:Species: Raphanus sativus (radish)
C:Date: 14-May-1999 #text_change 21-Jul-2000
C:Date: 14-May-1999 #text_change 21-Jul-2000
C:Accession: T07809
R:Sakamoto, K: Kusaba, M: Nishio, T.
Mol. Gen. Genet. 258, 397-403, 1998
A:Title: Polymorphism of the S-locus glycoprotein gene (SLG) and the S-locus related can be a second number: 216146; MuID:98311079
A:Recession: T07809
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Rociales: I-429 <SAK>
A:Rosidues: I-429 <SAK>
A:Cross-references: EMBL:AB009677; NID:93327839; PIDN:BAA31724.1; PID:93327840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:D85215; NID:92351161; PIDN:BAA21949.1; PID:92351162
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S-locus-specific glycoprotein - turnip (fragment)
N;Alternate names: S glycoprotein
C;Species: Barsaica rapa (turnip)
C;bate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C;Accession: T14415
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                             .,
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 429;
                                                                                                                                                                                                                                                                                          Length 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 GCRF-GTCTVQKLAHQIYQFTDKDKD------NVAPRSKISPQGY 52
                                                                                                                                                                                                                                                                                                                                             Indels
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Accession: A85489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                        Score 58.5; Di
Pred. No. 3.4;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 58.5; Di
Pred. No. 7.9;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 57.5; |
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                         25 KLAHQIYQFTD----KDKDNVAPRSKISPQG 51
                                                                                                                                                                            C;Genetics:
A;Gene: 20078
C;Superfamily: Escherichia coli yabP protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: 218078; MUID:97352858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.3%;
30.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 20.7%;
1 Similarity 32.7%;
16; Conservative 8
                                                                                                                                                                                                                                                                                     Query Match 20.7%;
Best Local Similarity 34.4%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-431 <KUS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: T14415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    echanism.
                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

ä

Gaps

5;

Indels

Length 712;

```
Myltcrnate names: tyrosinase (EC.114.10.1) Cintered (Species: Gallus gallus (chicken)
C; Species: Car. Kidson, S.H.
Gene 169, 191-195, 1996
A; Title: Characteristic sequences in the promoter region of the chicken tyrosinase-en A; Reference number: PC4153; MUID:96194800
A; Reference number: PC4153; MUID:96194800
A; Residues: 1-273 <FER>
A; Residues: 1-273 <FER>
A; Residues: 1-273 <FER>
A; Residues: 1-273 <FER>
A; Rocross-references: GB:L46805; NID:g1146320; PIDN:AAB08441.1; PID:g1146321
A; Note: The DNA sequence includes the first exon and a part of the first intron C; Comment: This enzyme is the rate-limiting enzyme in pigment blosynthesis.
C; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: monophenol monooxygenase
C; Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.1%; Score 57; DB 2; Length 273; 35.9%; Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
T14529
Flocus-specific glycoprotein - wild cabbage (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica oleracea (wild cabbage)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 NFQGLRSFGCRFG----TCTVQKL--AHQIYQFTDKDKD
```

```
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000 C; Accession: T14229
R; Kusbab, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A; Title: Striking sequence similarity in inter- and intra-specific comparisons of class echanism.
A; Reference number: 218078; MUID:97352858
A; Accession: T14229
A; Steference number: 218078; MUID:97352858
A; Accession: T14229
A; Steference number: 218078; MUID:97352858
A; Residues: 1-428 ACUS>
A; Residues: 1-428 ACUS>
A; Residues: 1-428 ACUS>
A; Residues: 1-428 ACUS>
A; Coss-references: ERBL:085205; NID:92351141; PIDN:BAA21939.1; PID:92351142
A; Molecule type: DNA
A; Residues: 1-428 ACUS>
A; Cross-references: ERBL:085205; NID:92351141; PIDN:BAA21939.1; PID:92351142
C; Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C; Keywords: glycoprotein
Ouery Match
Best Local Similarity 31.1%; Pred. No. 17;
Matches 19; Conservative 9; Mismatches 19; Indels 14; Gaps 3;
Apple 207 SGPQVHRSGPWNGVRFSGIPENQKLSYMVINFTENSEEVATTRWINNSFYSRLKVSSDG 266
Apple 267 Y 267
```

Search completed: October 17, 2002, 14:46:18 Job time : 6.96509 secs

THIS PAGE BLANK (USPTO)

```
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

October 17, 2002, 14:45:21; Search time 3.11222 Seconds (without alignments) 646.939 Million cell updates/sec Run on:

US-10-018-924-2\_COPY\_95\_146 283 1 YRQSMNNFQGLRSFGCRFGT......FTDKDKDNVAPRSKISPQGY Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	4		077559 canis famil	O62827 bos taurus	P43145 rattus norv	P97297 mus musculu	Q04604 rana nigrom		Q08410 coturnix co		P55024 gallus gall		Q28689 oryctolagus		P14679 homo sapien		P17252 homo sapien		P10102 oryctolagus		P54834 canis famil	_	O06491 bacillus su	Q01198 pseudomonas	P07065 bacteriopha	Q00341 homo sapien	Q9tlv1 bacteriopha	trionyx s	shigell	-	-	_	P05432 rattus norv
SUMMARIES		αı	ADML_HUMAN	ADML_PIG	ADML_CANFA	ADML_BOVIN	ADML_RAT	ADML_MOUSE	TYRO_RANNI	MRP2_RAT	TYRO_COTJA	MRP2_HUMAN	TYRO_CHICK	SYH_METTH	MRP2_RABIT	SLS6_BRAOL	TYRO_HUMAN	KPCA_BOVIN	KPCA_HUMAN	KPCA_MOUSE	KPCA_RABIT	KPCA_RAT	TYRO_CANFA	FGL2_HUMAN	GATA_BACSU	LIGD_PSEPA	TOP5_BPT4	VGLN_HUMAN	VG48_BPMU	TYRO_TRISI	MXID_SHIFL	MXID_SHISO	ENV_SFV1	MRP4_HUMAN	G33_RAT
		DB :	7	-	-	-	7	г	7	П	7	٦	-	-	-	-	г	7	Н	7	7	7	7	г		-	-	7	-	Н	Н	Н	-	-	-
		Match Length	185	188	188	188	185	184	532	1541	273	1545	529	425	1564	436	529	672	672	672	672	672	273	439	485	305	442	1268	180	273	266	266	982	1325	459
đ	Query	Match	_			92.9				21.6	20.8	20.8	20.1	19.4	19.4	19.3	18.7	18.7	18.7	18.7	18.7	18.7	18.4	18.4	18.4	18.2	18.2	18.2	18.0	18.0	18.0	18.0	18.0	18.0	17.8
		Score	283	277	265	263	231	222	65.5		59		57	52	52	54.5	53			53	53	53	52	52	2	•	51.5		51	51	51	51	51	51	50.5
	Result	No.	1	7	m	4	2	9	7	8	σ.	. 10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

	P31937 homo sapien P30470 homo sapien							
<u> </u>	<u></u>	<u>а</u> С	<b>*</b> *	Δ.	a	0	a	a
FUSE_DROME	D3HI_HUMAN 1B24_HUMAN	1B35_HUMAN	EYA3_HUMAN	RPOB_CHLMU	RPOB_CHLPN	RPOB_CHLTR	SOS1_MOUSE	SOS1_HUMAN
				-	_	-	-	<del>-</del>
805 922	336 354	362	573	1252	1252	1252	1319	1333
17.8	17.7	17.7	17.7	17.7	17.7	17.7	17.7	17.7
50.5	50 50	000	20	20	20	20	20	20
34 35	36	38	40	41	42	43	44	45

## ALIGNMENTS

```
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                         45
45
153
                                                                                                                                                                                                                                                                                                                                                                                                   110
                                                                                                         AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                         PEPTIDE
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                  PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                              PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADML_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               合
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                  SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN PHEOCHROMOCYTOMA AND ADRENAL MEDULLA. ALSO FOUND IN LUNG, VENTRICLE AND KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
         PITUITARY GLAND, BOTH PEPTIDES AT PHYSIOLOGICALLY RELEVANT DOSES INHIBIT BASAL ACTH SECRETION. BOTH PEPTIDES APPEAR TO ACT IN BRAIAND PITUITARY GLAND TO EXCLITARE THE LOSS OF PLASMA VOLUME, ACTIONS WHICH COMPLEMENT THEIR HYPOTENSIVE EFFECTS IN BLOOD
                                                                                                                                                                                                                                                                                                                                                                           PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
ADM precursor (Contains: Adrenomedullin (AM); Proadrenomedullin N-20 terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Adremal medulla; MEDLINE-94139945; PubMed-8043068; Ritamura K., Kangawa K., Kojima M., Ichiki Y., Matsuo H., Eto T.; Kicomplete amino acid sequence of porcine adrenomedullin and cloning of cDNA encoding its precursor."; FEBS Lett. 338:306-310(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                   AMIDATION (G-42 PROVIDE AMIDE GROUP). AMIDATION (G-147 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
Sus.
INHIBIT ALDOSTERONE SECRETION BY DIRECT ADRENAL ACTIONS. IN
                                                                                                                                                                                                                                                                                                                                                    Cleavage on pair of basic residues; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                  ADRENOMEDULLIN.
PREPROAM C-TERMINAL FRAGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YROSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               AMIDATION (G-147 PROVIDE A 64C7D2A0B4654DFE CRC64;
                                                                                                                  SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADM OR AM. (1919).
Suus scrofa (Pig).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 283; DB 1; 100.0%; Pred. No. 1.3e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                 InterPro; IPR001710; Adrenomedullin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                              EMBL; S73906; AAC60642.1; -.
EMBL; D43639; BAA07756.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                           Pfam; PF02039; Adrenomedullin; 1. PRINTS; PR00801; ADRENOMEDULN. Hormone; Amidation; Cleavage on pages
                                                                                                                                                                                                                                                                                                                                                                                                                                                           20420 MW;
                                                                                                                                                                                                                                    EMBL; D14874; BAA03589.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                   PIR, JN0476; JN0476.
PIR, JN0684; JN0684.
PIR; JC2351; JC2351.
MIM; 103275; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ma.
Local Sam.
52;
                                                                                                       TISSUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADML_PIG
P53366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA exerner
FEBS Let
                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                  PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                           PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                       PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                              PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADML_PIG
õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ono Y., Kojima M., Okada K., Kangawa K.; "CDNA cloning of canine adrenomedullin and its gene expression in the heart and blood vessels in endotoxin shock."; Shock 10:243-247(1998).
                                                                                                                                                                                                                                                                                                                                -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADRENAL GLANDS, LUNG, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proadrenomedullin N-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADML_CANFA STANDARD; PRT; 188 AA.
077559; 097769;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
ADM Precursor [Contrains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
BY SIMILARITY.
AMIDDATION (G-42 PROVIDE AMIDE GROUP).
AMIDDATION (G-147 PROVIDE AMIDE GROUP).
71749460F5660A61 CRC64;
                                                                                                                                                                                                                                       -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hormone, Amidation, Cleavage on pair of basic residues, Signal. SIGNAL _{\rm 1}
                                                                               Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y., Kawamoto M., Minamino N., Matsuo H., Eto T.;
"Identification and hypotensive activity of proadrenomedullin N-terminal 20 peptide (PAMP).";
FEBS Lett. 351:35-37(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 277; DB 1; Length 18
Pred. No. 8.6e-30;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of cDNA encoding canine adrenomedullin."; (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                              KIDNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADRENOMEDULLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Secreted
SEQUENCE OF 22-41.
TISSUE-Adrenal medulla;
MEDLINE-94357274; PubMed-8076689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-99002704; Pubmed-9788655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00801; ADRENOMEDULN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D14875; BAA03590.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 97.9
Best Local Similarity 98.1
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Imoto I., Jougasaki M.;
"Cloning of cDNA encodir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .146
188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115
41
146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
```

```
DISULFID
                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                             ADML_RAT
                                                                                                                                                                                                                                                    Ouery Match
                                                                                                              PEPTIDE
                                                                                                                                     PEPTIDE
                                                                                                                                                                                  MOD_RES
                                                                                                                                                                                                       MOD_RES
                                                                                                                         PROPEP
                                                                                                                                               PROPEP
                                                                                                                                                                                                                                                                                                                                                    ADML_RAT
   g
                                                                                                                                                                                                                                                                                                                                                                                         δy
                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                   ö
                               SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                           PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barker-S., Wood E., Clark A.J.L., Corder R.;
Cloning of bovine preproadrenomedullin and inhibition of its basal
expression in vascular endothelial cells by staurosporine.";
Life Sci. 62:1407-1415(1998).
                                                                                                                                                                                                                                                                                                          (BY SIMILARITY).
AMIDATION (G-147 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
 FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                   BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- FUNCTION: HYPOTENSIVE PEPTIDE. MAY FUNCTION AS A HORMONE IN
                                                                                                                                                                                                    Cleavage on pair of basic residues; Signal. 21 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                  PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                         22
                                                                                                                                                                                                                                                                                                                                                                           Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                       1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                     809D6A64F98F5578 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                            ; DB 1;
3.4e-28;
                                                                                                                                                                                                                                                                                                                                            (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 AA
                                                                                                                                                                                                                                                  ADRENOMEDULLIN
                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 3.46
0; Mismatches
                                                                                                                                                                                                                                       BY SIMILARITY
                                                                                                                                                                                                                                                                         SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CIRCULATION CONTROL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                             Score 265;
                                                                                                                                                                InterPro: IPR001710; Adrenomedullin. Pfam; PF02039; Adrenomedullin; 1. PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                                                                                                                                            ٠
۲
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                       Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Aorta;
MEDLINE-98244567; PubMed-9585168;
                                                                                                                                             EMBL; AF045773; AAD05423.1; -. EMBL; U96127; AAD09957.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                     20929 MW;
                                                                                                                                                                                                                                                                                                                                                                            93.6%;
94.2%;
                      SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                  49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                 146
188
                                                                                                                                                                                                                                                                                   115
                                                                                                                                                                                                                                                                                                                    146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              taurus (Bovine).
                                                                                                                                                                                                      Hormone; Amidation;
                                                                                                                                                                                                                                                                                                                                                       188 AA;
                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9913;
                                                                                                                                                                                                                                     45
95
148
                                                                                                                                                                                                                                                                                                                    146
                                                                                                                                                                                                                                                                                   110
                                                                                                                                                                                                                                                                                                47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADML_BOVIN
                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                           PEPTIDE
PROPEP
                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                 EPTIDE
                                                                                                                                                                                                                                                                                               MOD_RES
                                                                                                                                                                                                                                                                                                                    MOD_RES
                                                                                                                                                                                                                                                            PROPEP
                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADML_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                             g
ð
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang X., Yue T.L., Barone F.C., White R.F., Clark R.K., Willette R.N., Sulpizio A.C., Aiyar N.V., Ruffolo R.R. Jr., Fewerstein G.Z.; "Discovery of adrenomedullin in rat ischemic cortex and evidence for its role in exacerbating focal brain ischemic damage."; Proc. Natl. Acad. Sci. Us.A. 92:11480-11484(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matsuo H., Eto T.; Molecular cloning and biological activities of rat adrenomedullin, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                   PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor (Contains: Adrenomedullin (AM); Proadrenomedullin N-2(terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                          SIMITARITY).
BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
AMIDATION (G-147 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LUNG, KIDNEY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                Hormone, Amidation, Cleavage on pair of basic residues, Signal. SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93384621; PubMed-7690563;
Sakata J., Shimokuba T., Kitamura K., Nakamura S., Kangawa K.,
Matsuo H., Eto T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 YRQSLNNFQGLRSFGCRFGTCTVQKLAHQIYHFTDKDKDGSAPRSKISPQGY 146
                                                                                                                                                                                                                                                                                                                                                      PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3002E79AB3B6612C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: EXPRESSED IN ADRENAL GLANDS,
HEARY. SPLEEN, DUODENUM AND SUBMANDIBULAR GLANDS.
-!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypotensive peptide.";
Biochem. Biophys. Res. Commun. 195:921-927(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.9%; Score 263; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-SPRAGUE-DAWLEY; TISSUE-Adrenal gland;
                                                                                                                                                                                                                                                                                                                               ADRENOMEDULLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                  BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                   EMBL, AJ001613; CAA04866.1; -.
InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
MEDLINE=96102137; PubMed=8524787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20981 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                92
146
188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146
                                                                                                                                                                                                                                                                                                                                                                                                                                      41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                      22
45
95
148
                                                                                                                                                                                                                                                                                                                                                                                                            110
                                                                                                                                                                                                                                                                                                                                                                                                                                      41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146
```

```
PEPTIDE
                                                                                                                                                    PEPTIDE
                                                                                                                                                                                                 MOD_RES
                                                                                                                                                                                                                        MOD_RES
                                                                                                                                         PROPEP
                                                                                                                                                                PROPEP
                                                                                                                                                                                                                                                                                                                                                                                            TYRO_RANNI
                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                               g
   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                   ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation the Burposen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                       PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yotsumoto S., Ko M.S.H.;
"Expression of mouse adrenomedullin gene in trophoblastic glant cells at the implantation site.".
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                                   (BY SIMILARITY).
AMIDATION (G-144 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T., Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.; "Genomic organization, expression, and chromosomal mapping of the
                                                                                                                                                                                  SIMILARITY).
BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBL_TaxID=10090;
                                                                                                               Hormone; Amidation; Cleavage on pair of basic residues; Signal.
                                                                                                                                                                                                                                                                                                   ;;
                                                                                                                                                                                                                                                                                                                                   ADRENOMEDULLIN.
PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                                                                                                                                                                                                                                       1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
                                                                                                                                                                                                                                                       Score 231; DB 1; Lengt... -
                                                                                                                                                                                                                                                                           Length 185;
                                                                                                                                                                                                                                                   35CAD9A9DD19AE35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                 81.6%; Sco. No. 1...
84.6%; Pred. No. 1...
                                                                                                                                                    BY SIMILARITY.
                                                                                                                                                                                                                                           SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                     184 AA
                                                                                                                              SIMILARITY
                                                     EMBL; D15069; BAA03665.1; -.
EMBL; U15419; AAB60519.1; -.
INTERPRO; IPRO01710; Adrenomedullin.
PFEM; PF02039; Adrenomedullin; 1.
PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-129/SV;
MEDLINE-97092892; PubMed-8938454;
                                                                                                                                                                                                                                           (BY
                                                                                                                              BY
                                                                                                                                                                                                                                                                                                                                                                                                 ADML_MOUSE STANDARD;
P97297; P97453;
16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                      .,
Μ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse adrenomedullin gene."
Genomics 37:395-399(1996).
                                                                                                                                                                                                                                                      20636
                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                        185
                                                                                                                                                                                                           41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            musculus (Mouse).
                                                                                                                                                                                                                                                    185 AA;
                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                       22
45
94
149
                                                                                                                                                                                                                               143
                                                                                                                                                                                              107
                                                                                                                                                                                                          41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-C57BL/6J
                                                                                                                                                                                                                                                                                                  44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGENTS
                                                                                                                                                                                             DISULFID
MOD_RES
                                                                                                                                      PEPTIDE
PROPEP
                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                              PEPTIDE
                                                                                                                                                                                                                              MOD_RES
                                                                                                                              SIGNAL
                                                                                                                                                                       PROPEP
                                                                                                                                                                                                                                                                                                                                                                                          ADML_MOUSE
                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADM
                                                                                                                                                                                                                                                                                                                                                                              RESULT
ò
                                                                                                                                                                                                                                                                                                                                           ద
```

```
ï
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miura I., Okumoto H., Makino K., Nakata A., Nishloka M.;
"Analysis of the tyrosinase gene of the Japanese pond frog, Rana nigromaculata: cloning and nucleotide sequence of the genomic DNA containing the tyrosinase gene and its flanking regions.";
Jpn. J. Genet. 70:79-82(1995).
-i- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                         PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMIDATION (G-145 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rana nigromaculata (Japanese pond frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Amphibla; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
BY SINILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
                                                                                                                                                                                                                         Hormone; Amidation; Cleavage on pair of basic residues; Signal. SIGNAL 1 21 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nishioka M.;
tyrosinase of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 184;
                                                                                                                                                                                                                                                                                                                       ADRENOMEDULLIN.
PREPROAM C-TERMINAL FRAGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 222; DB 1; Lengtn 10-
Pred, No. 1.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> G (IN REF. 2).
C88C99045A79C898 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-93077054; PubMed-1446833;
Takase M., Miura I., Nakata A., Takeuchi T., I
"Cloning and sequencing of the cDNA encoding i
Papanese pond frog, Rana nigromaculata.";
Gene 121:359-363(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    532 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                   BY SIMILARITY
                                                                                                                   MGD; MGI:108058; Adm.
InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOPAGUINONE + H(2)O.
COFACTOR: BINDS TWO COPPER IONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95290234; PubMed-7772385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last seq
01-OCT-1996 (Rel. 34, Last anno
                                                                                                                                                                                                  PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.4%;
82.7%;
                                                                                                 EMBL; U77630; AAB36535.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-277 FROM N.A.
                                                                       EMBL; D78349; BAA11367.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                       144
184
                                                                                                                                                                                                                                                                                                                                                                                               113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144
                                                                                                                                                                                                                                                                                                                                                                                                                         41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                       22
45
95
151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-8409;
                                                                                                                                                                                                                                                                                                                                                                                               108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPOUNDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYR OR TYRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYRO_RANNI
                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
```

```
the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 QCQGNFWGYNCGECRFGYTGPNCTVRRNMIRRDIFRMTTAEKDKLIAYLNLA-KHTISP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 QSMNNFQGLRSFGCRFG----TCTVQK--LAHQIYQFTDKDKD-----NVAPRSKISP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MRP2_RAT STANDARD; PRT; 1541 AA.
063120; 063145;
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CT-2001 (Rel. 40, Last annotation update)
Canalicular multispecific organic anion transporter 1 (Multidrug resistance-associated protein 2) (Canalicular multidrug resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-WISTAR; TISSUE-Liver;
MEDLINE-96180672; PubMed-8599091;
Paulusma C.C., Bosma P.J., Zaman G.J.R., Bakker C.T.M., Otter M.,
Scheffer G.L., Scheper R.J., Borst P., Oude Elferink R.P.J.;
"Congenital jaundice in rats with a mutation in a multidrug
                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                          (GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                            . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Indels 13;
                                                                                                                                                                                                                                  TYROSINASE.
LUMENAL, MELANOSOME (POTENTIAL).
POTENTIAL.
                                                                                                                         InterPro; IPR002227; Tyrosinase.
Pfam; PR0064; tyrosinase; 1.
PRINTS; PR00092; TYROSINASE.
PROSITE; PS00497; TYROSINASE.1; 1.
PROSITE; PS00498; TYROSINASE.2; 1.
Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal; Transmembrane; Melanin blosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 532;
                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
COPPER A (BY SIMILARITY).
COPPER A (BY SIMILARITY).
COPPER B (BY SIMILARITY).
COPPER B (BY SIMILARITY).
COPPER B (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B27D3080F0C74B3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.1%; Score 65.5; DB 1; 33.9%; Pred. No. 0.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                            (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Mismatches
                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                          N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          resistance-associated protein gene."; Science 271:1126-1128(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-WISTAR; TISSUE-Liver;
MEDLINE-96279006; PubMed-8662992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein).
ABCC2 OR CMOAT OR MRP2 OR CMRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60115 MW;
                                                                                EMBL; D12514; BAA02077.1; -. EMBL; D37779; BAA07034.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20; Conservative
                                                                                                                                                                                                                                                                                                                                               371
394
90
1115
1165
                                                                                                              PIR; JC1392; JC1392.
                                                                                                                                                                                                                                   20
476
500
500
184
184
215
371
394
391
115
315
375
375
375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                   CHAIN
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                         METAL
METAL
                                                                                                                                                                                                                                                                                                                    METAL
METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                            STRAIN=SPRAGUE-DAWLEY; TISSUE-Liver; Ito K., Shimizu T., Sugiyama Y.; Ito K., Suzuki H., Hirohashi T., Kume K., Shimizu T., Sugiyama Y.; Expression of the putative ATP-binding cassette region, homologous to that in multidrug resistance associated protein (MRP), is hereditarily defective in Elsai hyperbillirubinemic rats (EHBR)."; Int. Hepatol. Commun. 292.292-299 (1996).
                                                                                                                                                                                                            ANIONS.
--- SUBCELLUAR LOCATION: Integral membrane protein.
--- TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE LIVER.
--- IDISEASE: DEFECTS IN ABCC2 ARE A CAUSE OF HEREDITARY CONJUGATED HYPERBILIRUBINEMIA (EHBR).
--- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
                          CDNA cloning of the hepatocyte canalicular isoform of the multidrug
Buechler M., Koenig J., Brom M., Kartenbeck J., Spring H., Horie T.,
                                        resistance protein, cMrp, reveals a novel conjugate export pump deficient in hyperbilirubinemic mutant rats.";
J. Biol. Chem. 271:15091-15098(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
5 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
6 (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 (BY SIMILARITY).
7 (BY SIMILARITY).
8 (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
9 (BY SIMILARITY).
10 (BY SIMILARITY).
10 (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP-binding: Glycoprotein; Transmembrane; Transport; Repeat.

DOMAIN
1 26 EXTRACELLULAR (BY SIMILARITY).
TRANSMEM 27 1 (BY SIMILARITY).
TRANSMEM 68 88 2 (BY SIMILARITY).
DOMAIN 69 92 EXTRACELLULAR (BY SIMILARITY).
TRANSMEM 93 113 3 (BY SIMILARITY).
DOMAIN 114 125 CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (BY SIMILARITY).
13 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (BY SIMILARITY).
12 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003439; ABC_transporter_tmem.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
Pfam; PF00064; ABC_membrane; 2.
Pfam; PF00005; ABC_tran; 2.
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00211; ABC_TRANSPORTER; 1
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, L49379, AAC42087.1; --
EMBL, X96393, CAA65257.1; --
EMBL, D86086; BAA13016.1; --
HSSP; P13569; INBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR003593; AAA.
Interpro; IPR001140; ABC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1029
1050
1093
1114
1115
1115
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1030
1051
1094
11115
11116
              Keppler D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-93181407; PubMed=1292011;
MEDLINE-93181407; PubMed=1292011;
MEDLINE-93181407; PubMed=1292011;
MEDLINE-93181407; PubMed=1292011;
MEDLINE-93181407; Masuko N., Miura H., Sato S., Tanaka M.,
Tanaka S., Takeuchi S., Shibahara S., Takeuchi T.;
Phylogeny of regulatory regions of vertebrate tyrosinase genes.";
THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC COMPOUNDS. CAPLAYZES THE RATE-LIMITING CONVERSIONS OF TYROSINE TO DOPA, DOPA TO DOPA—QUINONE AND POSSIBLY 5,6-DIHYDROXYINDOLE TO INDOLE-5,6 QUINONE.

-I- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coturnix coturnix japonica (Japanese quail),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                        17 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).

ATP (POTENTIAL).

ATP (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

M -> V (IN REF. 3).

M -> V (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOPAGUINONE + H(2)0.
COACACOR: BINDS TWO COPPER IONS.
SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.
SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-WV-1997 (Rel. 35, Last annotation update)
T<u>Y</u>rosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00264; tyrosinase.
PROSITE; PS00497; TYROSINASE_1; 1.
PROSITE; PS00497; TYROSINASE_1; 1.
OXIGOTED: PS00499; TYROSINASE_2; PRATIAL.
OXIGOTED: PS00499; TYROSINASE_2; PRATIAL.
TYRORIMED THE TYROSINASE_2; PRATIAL.
TYRORIMED THE TYROSINASE_2; PRATIAL.
TYRORIMED THE TYROSINASE SIGNAL
TYRORIMED THE TYROSINASE SIGNAL
TYROSINASE THE TYROSINASE SIGNAL
TYROSINASE THE TYROSINASE THE
                                                                                                                                                                                                                                                                                                                                                                                           Score 61; DB 1; Length 1541;
Pred. No. 4.8;
                                                    EXTRACELLULAR (BY SIMILARITY).
  CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                            SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 FGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQG
                                                                                                                                                                                                                                                                                                                                                                                        21.6%;
38.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S56788; AAB25510.1; -.
                                                                                                                                                                                                                                                                                                                                       173383
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                    1230
1251
1541
674
1337
                                                                                                                                                                                               1007
1010
1011
420
                                                                                                                                                                                                                                                1010 101
1011 101
420 42
1541 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=93934;
                                                                                                                                     667
1330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYRO_COTJA
Q08410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fragment).
                                                                                                                                  NP_BIND
NP_BIND
CARBOHYD
DOMAIN
TRANSMEM
                                                      DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
STIFFFFFFFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
```

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96390592; PubMed-8797578;
Taniguchi K., Wada M., Kohno K., Nakamura T., Kawabe T., Kawakami M.,
Kagotani K., Okumura K., Akiyama S., Kuwano M.;
"A human canalicular multispecific organic anion transporter (CMOAT)
gene is overexpressed in cisplatin-resistant human cancer cell lines
with decreased drug accumulation.";
Cancer Res. 56:4124-4129(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Kool M., de Haas M., Ponne N.J., Paulusma C.C., Oude-Elferink R.P.J.,
Baas F., Borst P.;
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              multidrug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-96279006; Pubmed-8662992;
Buechler M., Koenig J., Brom M., Kartenbeck J., Spring H., Horie T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-99395001; Pubmed-10464142;
Tsulil H., Koenig J., Rost D., Stoeckel B., Leuschner U., Kappler D.
"Exon-intron organization of the human multidrug-resistance protein (MRP2) gene mutated in Dubin-Johnson syndrome.";
Gastroenterology 117:653-660(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MRP2_HUMAN STANDARD; PRT; 1545 AA.
Q92887; Q99663; Q92798; Q14022; Q92500; Q9UMS2;
G15-UUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CT-2001 (Rel. 40, Last annotation update)
Canalicular multispecific organic anion transporter 1 (Multidrug resistance-associated protein 2) (Canalicular multidrug resistance
COPPER A (BY SIMILARITY).

COPPER A (BY SIMILARITY).

COPPER A (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Elvamo sapiens (Human).
Elvaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT DJS TRP-768.
MEDLINE-98087571; PubMed-9425227;
Wada M., Toh S., Taniguchi K., Nakamura T., Uchiumi T., Kohno K.,
Yoshida I., Kimura A., Sakisaka S., Adachi Y., Kuwano M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dwnd
                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      resistance protein, cMrp, reveals a novel conjugate export deficient in hyperbilirubinemic mutant rats."; J. Biol. Chem. 271:15091-15098(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA cloning of the hepatocyte canalicular isoform of the
                                                                                                                                                                                                                                                                                                    Score 59; DB 1; Length 273;
                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                          OEA3DE55BE11EA1A CRC64;
                                                                                                                                                                                                                                                                                                                                                              13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 NFQGLRSFGCRFG----TCTVQKL--AHQIYQFTDKDKD 39
                                                                                                                                                                                                                                                                                                                                Pred. No. 1.5;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABCC2 OR CMOAT1 OR CMOAT OR MRP2 OR CMRP.
                                                                                                                                                                                                                                             MM;
                                                                                                                                                                                                                                                                                                    20.8%;
35.9%;
                                                                                                                                                                                                                                             31499
                                                                                                                                                                                                                                                                                                                                Local Similarity 35.9
hes 14; Conservative
      202
202
211
211
86
1111
161
230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-1996)
                                                                                                                                                                                                                                          273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Keppler D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein).
                                                                                           CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                  NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Keppler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRP2_HUMAN
                                                                      METAL
                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                         Best
         SELLELLES
                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC DDT THE STANDARD THE STANDA
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                      CONJUGATED
"Mutations in the canilicular multispecific organic anion transporter (CMAT) gene, a novel ABC transporter, in patients with Myperbilitubinemia II/Dubin-Johnson syndrome."; Hum. Mol. Genet. 7:203-207(1998).
                                                                                                              MEDLINE-99162196; PubMed-10053008;
Toh S., Wada M., Uchiumi T., Inokuchi A., Makino Y., Horie Y.,
Adachi Y., Sakisaka S., Kuwano M.;
"Genomic structure of the canalicular multispecific organic anion-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR003593; AAA.
Interpro; IPR001140; ABC_transporter_tmem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOINED,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOINED
                                                                                                VARIANTS DJS TRP-768 AND ARG-1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AJ132244; CAB45309.1; AJ132244; CAB45309.1; June AJ132287; CAB45309.1; June AJ132289; CAB45309.1; June AJ132291; CAB45309.1; June AJ132292; June AJ132292; June AJ142292; June AJ142929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U63970; AAB39892.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAB45309.1;
CAB45309.1;
CAB45309.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, U49248; AAB09422.1;
EMBL, X96395; CAA65259.2;
EMBL, AJ132244; CAB45309.1;
EMBL, AJ132287; CAB45309.1;
EMBL, AJ132288; CAB45309.1;
EMBL, AJ132288; CAB45309.1;
EMBL, AJ13289; CAB45309.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AJ132309; CAB45309.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AJ132312; CAB45309.1;
AJ132313; CAB45309.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAB45309.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAB45309.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAB45309.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AJ132310; CAB45309.1;
AJ132311; CAB45309.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAB45309.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAB45309.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAB45309.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAB45309.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAB45309.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAB45309.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAB45309.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAB45309.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAB45309.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAB45309.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAB45309.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAB45309.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AJ132301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AJ132305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
```

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                       7 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
B (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
9 (BY SIMILARITY).
10 (BY SIMILARITY).
11 (BY SIMILARITY).
12 (BY SIMILARITY).
13 (BY SIMILARITY).
14 (BY SIMILARITY).
15 (BY SIMILARITY).
16 (BY SIMILARITY).
17 (BY SIMILARITY).
18 (BY SIMILARITY).
19 (BY SIMILARITY).
11 (BY SIMILARITY).
11 (BY SIMILARITY).
12 (BY SIMILARITY).
13 (BY SIMILARITY).
                                                                                                                                                           2 (BY SIMILARITY).

EXTRACELULAR (BY SIMILARITY).

3 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).

4 (BY SIMILARITY).

5 (BY SIMILARITY).

5 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (BY SIMILARITY).
14 (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
15 (BY SIMILARITY).
16 (BY SIMILARITY).
16 (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
                                                                          PORTER; 1.
Transmembrane; Transport; Repeat;
                                                                                                                EXTRACELLULAR (BY SIMILARITY).

1 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1545;
                                                                                                                                                                                                                                                                               6 (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTIG-VAR_000099.

Q -> R (IN DJS).

/FTIG-VAR_010756.

V -> E (IN REF. 2).

V -> G (IN REF. 5).

C -> Y (IN REF. 2).

C -> Y (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYRO_CHICK STANDARD; PRT; 529 AA. P55024; 01-007-1996 (Rel. 34, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 FGTCTVQKLAHQIYQFTDKDKDNVAPRSKI----SPQ 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 59; DB 1
Pred. No. 8.9;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R -> W (IN DJS)
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; APP_GTP_A.
Pfam; PP00664; ABC_membrane; 2.
Pfam; PF00005; ABC_tran; 2.
SNART; SN00382; AAA; 1.
PROSITE; SN00311; ABC_TRANSPORTER; 1.
ATP-binding; Glycoprotein; Transmembran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 20.8%;
Best Local Similarity 37.8%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1033
1054
1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1211
1232
1234
1255
1255
1545
678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1430
1515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
1011
768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1430 143
1515 151
1545 AA;
                                                                                                       Disease mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
CONFLICT
SEQUENCE
                                                                                                                     DOMAIN
TRANSMEM
                                                                                                                                                DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                        DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
                                                                                                                                                                                                          DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRANSMEM
                                                                                                                                                                                           FRANSMEM
                                                                                                                                                                                                                                                                                                             RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                 RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                   RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                             PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /ARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /ARIANT
                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                OMAIN
                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYRO_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22555
```

œ

```
(HisRS
                                           g
                  à
                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC COMPOUNDS. CATALYZES THE RATE-LIMITING CONVERSIONS OF TYROSINE TO DOPA, DOPA TO DOPA-QUINONE AND POSSIBLY 5,6-DIHYDROXYINDOLE TO INDOLE-5,6 QUINONE.

-1- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA +
                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).

COPPER A (BY SIMILARITY).

COPPER B (BY SIMILARITY).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                   Mochil M., Ilo A., Yamamoto H., Takeuchi T., Eguchi G.; "Isolation and characterization of a chicken tyrosinase cDNA."; Pigment Cell Res. 5:162-167(1992).
                                                                                                                                                                                                                                                  "Characteristic sequences in the promoter region of the chicken tyrosinase-encoding gene."; Gene 169:191-195(1996).
                                                                                                                                                                                                                                                                                                                                                                                     -1- COFACTOR: BINDS TWO COPPER IONS.
-1- SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.
-!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.
Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal; Transmembrane; Melanin biosynthesis.
SIGNAL 1 18 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LUMENAL, MELANOSOME (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 20.1%; Score 57; DB 1; Length 529; Best Local Similarity 35.9%; Pred. No. 5.4; Matches 14; Conservative 5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74B464A52C3EFBF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYROSINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D88349; BAA13590.1; --
EMBL; L46805; AAB08441.1; --
InterPro; IPR00227; Tyrosinase.
Pfam; PF00264; tyrosinase; 1.
PRNYTS; PR00092; TYROSINASE;
PROSITE; PS00497; TYROSINASE_1; 1.
PROSITE; PS00498; TYROSINASE_2; 1.
                                                                                                       SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN;
MEDLINE-93157254; Pubmed-1494538;
                                                                                                                                                                                                           SEQUENCE OF 1-273 FROM N.A. MEDLINE-96194800; Pubmed-8647445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60357 MW;
                                                                                                                                                                                                                                     Ferguson C.A., Kidson S.H.;
                           Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371
529 AA;
                                                                                NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METAL
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
```

; ;

Gaps

;

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
-!- CATALYTIC ACTILYTY: ATP + L-histidine + tRNA(His) = AMP +
dlphosphate + L-histidyl-tRNA(His).
-!- SUBCELLUTAR LOCATION. Cytoplasanic.
-!- SIMILARITY: BELONGS TO CLASS-1I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00179; AA_TRNA_LIGASE_II_1; FALSE_NEG.
PROSITE; PS00339; AA_TRNA_LIGASE_II_2; FALSE_NEG.
Aminoacyl-trnA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee H.-M., Dubois J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Kaale P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pletrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; Complete genome sequence of Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.4%; Score 55; DB 1; Length 425; 31.7%; Pred. No. 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        425 AA; 48019 MW; 8388A5975A017535 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 FQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKIS 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 NFQGLRSFGCRFG----TCTVQKL--AHQIYQFTDKDKD 39
                                                                                                                                                                                                                                     425 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, 032422; 1QE0.
InterPro; IPR002106; AA_tRNA_ligase_II.
InterPro; IPR004154; HGTP_anticodon.
InterPro; IPR002314; tRNA-synt_2b.
Pfam; PF03129; HGTP_anticodon; I.
Pfam; PF03129; tRNA-synt_2b; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000811; AAB84750.1; ALT_INIT
                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-DELTA H;
MEDLINE-98037514; PubMed-9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 19.4%
Best Local Similarity 31.7%
Matches 13; Conservative
                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=145262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome
SEQUENCE 425 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HISS OR MTH244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MRP2_RABIT
Q28689;
                                                                                                                                                                                                                                 SYH_METTH
026346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
MRP2_RABIT
```

```
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
                                                                                                                                                                                                                        chloride

    1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
    1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY AND SMALL

30-MXY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Canalicular multispecific organic anion transporter 1 (Multidrug resistence-associated protein 2) (Canalicular multidrug resistance protein) (Epithelial basolateral chloride conductance regulator).
ABCC2 OR MRP2 OR EBCR.
                                                                                                                                                                                           van Kuijck M.A., van Aubel R.A.W.H., Busch A.E., Lang F., Russel F.G.W., Bindels R.J.W., van Os C.H., Deen P.M.T.; Molecular cloning and expression of a cyclic AMP-activated chloric conductance regulator: a novel ATP-binding cassette transporter."; Proc. Natl. Acad. Sci. U.S.A. 93:5401-5406(1996).
                                                                                                                                                                                                                                                                                  MEDIINE-98279125; PubMed-9614209;
van Aubel R.A.M.H., van Kuijck M.A., Koenderink J.B., Deen P.M.T.,
van Os C.H., Russel F.G.M.;
                                                                                                                                                                                                                                                                                                                                                                             -1- FUNCTION: MEDIATES HEPATOBILIARY EXCRETION OF NUMEROUS ORGANIC
                                                                                                                                                                                                                                                                                                                          Adenosine triphosphate-dependent transport of anionic conjugates
                                                                                                                                                                                                                                                                                                                                         the rabbit multidrug resistance-associated protein Mrp2 expressed
                                                                                     Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat.

DOMAIN 1 27 EXTRACELLULAR (BY SIMILARITY).

TRANSMEM 28 48 1 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (NY SIMILARITY).
2 (BY SIMILARITY).
2 (BY SIMILARITY).
3 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
5 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (BY SIMILARITY).
7 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
8 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
9 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (BY SIMILARITY).
6 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001140; ABC_transporter_tmem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (BY SIMILA CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_A.
Pfam: PF00064; ABC_membrane; 2.
SMART; SM00382; ABC_tran; 2.
SMART; SM0382; AAA; 2.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
                                                                                                                                                                                                                                                                                                                                                                Mol. Pharmacol. 53:1062-1067(1998)
                                                                                                                                                                   TISSUE=11eum;
MEDLINE-96224297; PubMed-8643587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 249144; CAA89004.1; -. HSSP; P13569; 1NBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003593; AAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147
165
186
                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                              NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                   INTESTINE
                                                                                                                                                                                                                                                                                                                                                    cells.
                                                                                                                                                                                                                                                                                                                                                                                        ANIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                       FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nastallah J.B., Kao T.-H., Goldberg M.L., Nastallah M.E.;
Nature 326:523-523(1987).
-!- FUNCATION: INVOLVED IN SPOROPHYTIC SELF-INCOMPATIBILITY SYSTEM
(THE INABILITY OF FLOWERING PLANTS TO ACHIEVE SELF-FERTILIZATION).
-!- TISSUE SPECIFICITY: STICKAA.
-!- POLYMORPHISM: THERE ARE A TOTAL OF 50 DIFFERENT S ALLELES IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nasrallah J.B., Kao T.-H., Chen C.H., Goldberg M.L., Nasrallah M.E.; "Amino-acid sequence of glycoproteins encoded by three alleles of the S locus of Brassica oleracea."; Nature 386:617-619(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nasrallah J.B., Kao T.-H., Goldberg M.L., Nasrallah M.E.;
"A cDNA clone encoding an S-locus-specific glycoprotein from Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                             ATP (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. .) (POTENTIAL)
W; D8FBF5AC8FE45873 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: TO THE EXTRACELLULAR PORTION OF A MAIZE PROTEIN KINASE RECEPTOR (ZMPK1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                10 (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
11 (BY SIMILARITY).
                                                                                              12 (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
13 (BY SIMILARITY).
                                                                                                                                                                                        EXTRACELLULAR (BY SIMILARITY).
15 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                    EXTRACELLULAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 1564;
                                                                          CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                    CYTOPLASMIC (BY SIMILARITY).
14 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                        17 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Indels
    CYTOPLASMIC (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
S-locus-specific glycoprotein S6 precursor (SLSG-6).
                                                                                                                                                                                                                                                  16 (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 FGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brassica oleracea (Cauliflower).
                                                                                                                                                                                                                                                                                                                                                                                                                         175542 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 22-435 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 318:263-267(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                              1031
1052
11052
11116
11117
11138
11230
11232
11232
11233
11243
1243
1243
1243
                                                                                                                                                                                                                                                                                                                                                                                                       1009
                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     1009
1564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3712;
                                                                                                                991
1032
1053
1096
                                                                                                                                                                                                            1118
1139
1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B.OLERACEA.
                                                                                                                                                                                                                                                                        231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLS6_BRAOL
P07761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oleracea.
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                      TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                          DOMAIN
TRANSMEM
                                                                                                                                                                                                                                DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                               NP_BIND
CARBOHYD
                                                                                                              DOMAIN
TRANSMEM
                                                                                                                                                    DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERRATUM
                                                                                                                                                                                                                                                                                                                               NP_BIND
                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
SLS6_BRAOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
```

ö

```
Bouchard B.,
  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                              ;
;
the European Bioinformatics Institute. There are no restrictions on
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDINE-91236163; PubMed-1903356; Giebel L.B., Strunk K.M., Spritz R.A.; "Organization and nucleotide sequences of the human tyrosinase gene and a truncated tyrosinase-related segment.";
                                                                                                                                                                                                                N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-88041128; PubMed=2823263; Kwon B.S., Haq A.K., Pomerantz S.H., Halaban R.; Isolation and sequence of a cDNA clone for human tyrosinase that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYROLHUMAN STANDARD; PRT; 529 AA.
P14679; Q15676; Q15675; Q15680;
01-APR-1990 (Rel. 14, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase)
(Tumor rejection antigen AB) (SK29-AB) (LB24-AB).
                                                                                                                                                                                                        S-LOCUS-SPECIFIC GLYCOPROTEIN S6.
                                                                                                                                                                                                                                                                                                                      19.3%; Score 54.5; DB 1; Length 436; 28.6%; Pred. No. 9.6;
                                                                                                                                                                                                                                                                                                                                                                              227 GVRFSGIPEDQKLSYMVYNFTENSEEVAYTFRMTNNSIYSRLTLSSEGY 275
                                                                                                                                                                                                                                                                                                                                                                  15 GCRF-GTCTVQKLAHQIYQFTDKDKD------NVAPRSKISPQGY 52
                                                                                                                                                                                  Glycoprotein; Polymorphism; Signal.
                                                                                                                                                                                                                                                                                                                                            14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 84:7473-7477(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kwon B.S., Hag A.K., Pomerantz S.H., Halaban R.;
Proc. Natl. Acad. Sci. U.S.A. 85:6352-6352(1988)
                                                          -----------------------
                                                                                                                                                                                                                                                                                                                                           10; Mismatches
                                                                                                                                                                                             POTENTIAL.
                                                                                     PIR; A27827, A27827.
InterPro; IPR001480; B_lectin.
InterPro; IPR003609; Pan_app.
InterPro; IPR000858; Slocus_glycop.
                                                                             EMBL; X03170; CAA26934.1; ALT_INIT
                                                                                                                                  Pfam: PF01453; Agglutinin; 1. Pfam: PF00954; S. Locus glycop; 1. Swarr; SW00108; B_lectin; 1. SWART; SW00473; PAN_AP; 1. Self-incompatibility; Glycoprotei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        maps at the mouse c-albino locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-Melanoma;
MEDLINE-89279151; Pubmed-2499655;
                                                                                                                                                                                                                                                                                               49779 MW;
                                                                 EMBL; Y00268; CAA68375.1; -
                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomics 9:435-445(1991).
                                                                                                                                                                                             31
436
46
64
1114
121
261
390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS TO 384-398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                  121
245
261
390
436 AA;
                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
g
                                                                                                                                                                                                                                                                                                                                                                   à
```

```
Oetting W.S.; King R.A.; "Molecular basis of type I (tyrosinase-related) oculocutaneous albinism: mutations and polymorphisms of the human tyrosinase gene."; Hum. Mutat. 2:1-6(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spritz R.A., Strunk K.M., Glebel L.B., King R.A.; "Detection of mutations in the tyrosinase gene in a patient with type
                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-91271371; Pubmed-1711223;
Chintamaneni C.D., Halaban R., Kobayashi Y., Witkop C.J., Kwon B.S.;
"A single base insertion in the putative transmembrane domain of the tyrosinase gene as a cause for tyrosinase-negative oculocutaneous albinism.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Liver;
MEDLINE-90089403; PubMed-2480811;
KIKUChi H., Miura H., Yamamoto H., Takeuchi T., Dei T., Watanabe M.;
"Characteristic sequences in the upstream region of the human tyrosinase gene.";
Blochim. Biophys. Acta 1009:283-286(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-90238992; PubMed-1970634;
Giebel L.B., Strunk K.M., King R.A., Hanifin J.M., Spritz R.A.;
"A frequent tyrosinase gene mutation in classic, tyrosinase-negative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-91241133, PubMed-1903591;
Giebel L.B., Tripathi R.K., Strunk K.M., Hanifin J.M., Jackson C.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Melanoma, and T-cell;
MEDLINE-33440625; PubMed-340755;
Brichard V., van Woelfel T., Woelfel C., de Plaen E.,
Lethe B., Coulle P., Boon T.;
"The tyrosinase gene codes for an antigen recognized by autologous cytolytic T lymphocytes on HLA-A2 melanomas.";
J. EXP. Med. 1781489-495(1993).
Souchard B., Fuller B.B., Vijayasaradhi S., Houghton A.N.;
Induction of pigmentation in mouse fibroblasts by expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Tyrosinase gene mutations associated with type IB ('yellow') oculocutaneous abbinsm."; Am. J. Hum. Genet. 48:1159-1167(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANTS TYR-192; GLN-402; OCA-IA LYS-373 AND OCA-IA ASN-383.
MEDLINE-90259036; Pubmed=2342539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-32 FROM N.A. MEDLINE-89351001; PubMed-2504160; Takeda A., Tomita Y., Okinaga S., Tagami H., Shibahara S.; "Functional analysis of the CDNA encoding human tyrosinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Octting W.S., King R.A.; Molecular basis of albinism: mutations and polymorphisms pigmentation genes associated with albinism."; Hum. Mutat. 13:99-115(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 88:5272-5276(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 162:984-990(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (type IA) oculocutaneous albinism.";
Proc. Natl. Acad. Sci. U.S.A. 87:3255-3258(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IA oculocutaneous albinism.";
New Engl. J. Med. 322:1724-1728(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS OCA-IB PHE-275 AND LEU-406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-99140254; PubMed-10094567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVIEW ON OCA VARIANTS.
MEDLINE=93237884; PubMed=8477259;
                                                                              human tyrosinase cDNA.";
J. Exp. Med. 169;2029–2042(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-272 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVIEW ON OCA-I VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT OCA-IA LEU-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
```

```
Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Holmes S.A., Spritz R.A.; "Mutations of the tyrosinase gene in Indo-Pakistani patients with type I (tyrosinase-deficient) oculocutaneous albinism (OCA)."; Am. J. Hum. Genet. 53:1173-1179(1993).
                                                                                                                                                                                                                                                                                                                                                    VARIANT OCA-ITS GLN-422.
MEDLINE=91154384; PubNed=1900309;
Giebel L.B., Tripathi R.K., King R.A., Spritz R.A.;
A tyrosinase gene missense mutation in temperature-sensitive type I coulcoutaneous albinism. A human homologue to the Siamese cat and the Himalayan mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Breimer L.H., Winder A.F., Jay B., Jay M.; "Initiation codon mutation of the tyrosinase gene as a cause of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS OCA-IA D-47; C-217 DEL; H-299 AND K-373, AND VARIANTS OCA-IB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Octting W.S., King R.A.; "Molecular analysis of type I-A (tyrosinase negative) oculocutaneous
                                                                                                                            Tripathi R.K., Strunk K.M., Glebel L.B., Weleber R.G., Spritz R.A.; "Tyrosinase gene mutations in type I (tyrosinase-deficient) coulocutaneous albinism define two clusters of missense substitutions.";
     Giebel L.B., Tripathi R.K., Strunk K.M., Hanifin J.M., Jackson C.E.
King R.A., Spritz R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-94070862; PubMed-7902671;
Tripathi R.K., Bundey S., Musarella M.A., Droetto S., Strunk K.M.,
Holmes S.A., Spritz R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gershoni-Baruch R., Rosenmann A., Droetto S., Holmes S.,
Tripathi R.K., Spritz R.A.;
"Mutations of the tyrosinase gene in patients with oculocutaneous
albinism from various ethnic groups in Israel.";
Am. J. Hum. Genet. 54:586-594(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS OCA-IA ARG-361 AND TYR-371.
MEDLINE-96243675; PubMed-8644824;
Summers C.G., Octting W.S., King R.A.;
"Diagnosis of coulocutaneous albinism with molecular analysis.";
Am. J. Ophthalmol. 121:724-726(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS OCA TYR-367; THR-370 AND LYS-373, AND VARIANT GLN-402. MEDLINE-95043421; PubMed=7955413;
                                                                                                                                                                                                                                                MEDLINE-91118940; PubMed-1899321;
Spritz R.A., Strunk K.M., Hsieh C.-L., Sekhon G.S., Francke U.; *Homozygous tyrosinase gene mutation in an American black with tyrosinase-negative (type IA) oculocutaneous albinism.";
Am. J. Hum. Genet. 48:318-324(1991).
                                                                             VARIANTS OCA-IA SER-21; TRP-217; HIS-299; SER-403; SER-446 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92048465; PubMed-1943686;
King R.A., Mentink M.M., Oetting W.S.;
"Non-random distribution of missense mutations within the hume
tyrosinase gene in type I (tyrosinase-related) oculocutaneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS OCA-IA GLY-42; TYR-55; THR-206 AND ARG-419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS OCA-IA GLN-328; ARG-419 AND LEU-431
                                             J. Hum. Genet. 49:696-696(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARIANTS OCA-IA ILE-176 AND GLN-217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clin. Invest. 87:1119-1122(1991).
                                                                                                                                                                                                  Am. J. Med. Genet. 43:865-871(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S-152 AND K-294.
MEDLINE-94175072; PubMed-8128955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93138611; PubMed=1487241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clin. Chim. Acta 227:17-22(1994).
                                                                                                                MEDLINE=92351982; PubMed=1642278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol. Biol. Med. 8:19-29(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jum. Genet. 90:258-262(1992).
                                                                                                                                                                                                                                    VARIANT OCA-IA ARG-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                albinism.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              albinism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            albinism.
```

```
"Apparent digenic inheritance of Waardenburg syndrome type 2 (WS2) and autosomal recessive ocular albinism (AROA).";
Hum. Mol. Genet. 6:659-664(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                           MEDLINE-97403941; PubMed=9259202;
Spritz R.A., Oh J., Fukai K., Holmes S.A., Ho L., Chitayat D.,
France T.D., Musarella M.A., Orlow S.J., Schnur R.E., Weleber R.G.,
                                        Morell R., Spritz R.A., Ho L., Pierpont J., Guo W., Friedman T.B.,
Asher J.H. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 529;
19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18; Indels
                                                                                                                                                                                                                                                                                         Levin A.V.;
"Novel mutations of the tyrosinase (TYR) gene in type I occulocutaneous albinism (OCA1).";
Hum. Mutat. 10:171-174(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 OCSGNFMGFNCGNCKFGFWGPNCTERRLLVRRNIFDLSAPEKD 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 QSMNNFQGLRSFGCRFG----TCTVQKL--AHQIYQFTDKDKD 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: October 17, 2002, 14:49:13 Job time : 4.11222 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                    Oetting W.S., Fryer J.P., King R.A.;
                      MEDLINE=97301760; PubMed=9158138;
                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS OCA-IA AND OCA-IB.
                                                                                                                                                                                            VARIANTS OCA-IA AND OCA-IB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 13; Conserv
VARIANT GLN-402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
```

5

THIS PAGE BLANK (USPTO)

```
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

October 17, 2002, 15:20:12; Search time 9.48534 Seconds (without alignments) 742.931 Million cell updates/sec :: 0

Run

US-10-018-924-2\_COPY\_4\_185 947 Title:

1 VSVALMYLGSLAFLGADTAR.....SKPQAHGAPAPPSGSAPHFL 182 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries Maximum Match 100%

SwissProt\_40:\* Database: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# OUT CLASSICAL CO.

		Description	P35318 homo sapien	P53366 sus scrofa	pos	. 077559 canis famil	P43145 rattus norv	P97297 mus musculu		P12259 homo sapien		Q01338 mus musculu	P27902 streptomyce		P22909 rattus norv	Q16650 homo sapien		P30640 caenorhabdi	P47973 rattus norv					-		Q62311 mus musculu	O13559 saccharomyc	P40105 saccharomyc	P53345 saccharomyc	P53819 saccharomyc	P41593 mus musculu	Q63801 rattus norv	Н	Q64336 mus musculu	P29129 pseudorabie
SUMMARIES		DI .	ADML_HUMAN	ADML_PIG	ADML_BOVIN	ADML_CANFA	ADML_RAT	ADML_MOUSE	TTP_HUMAN	FA5_HUMAN	CEFD_STRCL	A2AA_MOUSE	DNAA_STRCO	MPI2_RAT	A2AA_RAT	TBR1_HUMAN	REPA_AGRTU	YNE1_CAEEL	TTP_RAT	A2AA_HUMAN	KR1_HSV2H	VP40_SCMVC	YRF1_YEAST	CYAA_PODAN	GAG_SIVAT	T2D5_MOUSE	YRF4_YEAST	YRF2_YEAST	YRF3_YEAST	YRF6_YEAST	PTRR_MOUSE	T2D5_RAT	A2AA_PIG	TBR1_MOUSE	ICPO_PRVIF
		Length DB	185 1	188 1	188 1	188	185 1	184 1	326 1	2224 1	397 1	450 1	656 1	574 1	450 1	682 1	250 1	458 1	320 1				1796 1					1681 1						_	410 1
ф		Match L	100.0	86.3	81.8	81.4	62.3	60.2				9.2	٠.		8.7		٠.	8.4		•		•	8.3	•		•		•		•	•				8.0
		Score	947	817	774.5	771	624.5	570	89.5	89	88.5	87	87	83.5	82	80.5	80	80	79	79	78.5	78.5	78.5	78.5	78	78	77.5	77.5	77.5	77.5	77	77	76.5	76.5	16
	Result	No.	Н	7	ю	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

Q61315 mus musculu P22893 mus musculu P41969 mus musculu P25661 rattus norv P28284 herpes simp P32337 saccharonyc P10092 homo sapien P53781 bos taurus Q9hc52 homo sapien P06401 homo sapien Q07998 brachydanio O54898 rattus norv
APC_MOUSE ELEKI_MOUSE BELKI_MOUSE PTRE_RAT ICPO_HSV2H ICMO_LSV2H ICMOUSE CALZ_HUWAN TTP_BOVIN TTP_BOVIN BRAC_BRARE GRAC_BRARE CCAG_RAT
апанананана
2845 3199 4219 5591 1089 1089 324 389 933 423
8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
75 7.5 7.5 7.5 7.4 7.5 7.4 7.5 7.4 7.5
44444444444444444444444444444444444444

## ALIGNMENTS

```
MEDLINE-20053666; PubMed-10588445;
Champion H.C., Nussdorfer G.G., Kadowitz P.J.;
Regul. Pept. 85:1-8(1999).
-: FONCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR AGENTS. NUMEROUS ACTIONS HAVE BEEN REPORTED MOST RELATED TO THE PHYSIOLOGIC CONTROL, OF FLUID AND ELECTROLYTE HOMEOSTASIS. IN THE KIDNEY, AM IS DIURETIC AND NATRIURETIC, AND BOTH AM AND PAMP
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-Pheochromocytoma;
MEDLINE-9334928; PubbMed-7688224;
Kitamura K., Sakata J., Kangawa K., Kojima M., Matsuo H., Eto T.;
"Cloning and characterization of cDNA encoding a precursor for human
                                                               01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor (Contains: Adrenomedullin (AM); Proadrenomedullin N-20 terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matsuo H., Eto T.;
"Adrenomedullin: a novel hypotensive peptide isolated from human pheochromocytoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Nakamura S.,
Matsuo H., Eto T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-94354869; PubMed-8074714;
Ishimitsu T., Kojima M., Kangawa K., Hino J., Matsuoka H., Kitamura K., Eto T., Matsuo H.;
"Genomic structure of human adrenomedullin gene.";
Blochem. Biophys. Res. Commun. 203:631-639(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 192:553-560(1993).
                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 194:720-725(1993).
                                   185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Samson W.K.; "Proadrenomedullin-derived peptides."; Front. Neuroendocrinol. 19:100-127(1998).
                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Pheochromocytoma; MEDLINE=93249425; PubMed=8387282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98240137; PubMed=9578982;
                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 95-146.
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              adrenomedullin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Liver
                                 ADML_HUMAN
                                                                                                                                                               ADM OR AM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVIEW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVIEW
RESULT 1
ADML_HUMAN
```

```
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADML_BOVIN
ID ADML.
AC OF DT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMIG outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
INHIBIT ALDOSTERONE SECRETION BY DIRECT ADRENAL ACTIONS. IN PRIUTARY GLAND, BOTH PRETIDES AT PHYSICLOGICALLY RELEVANT DOSES INHIBIT BASAL ACTH SECRETION. BOTH PEPTIDES APPEAR TO ACT IN BRAIN AND PITUTARY GLAND TO FACILITATE THE LOSS OF PLASMA VOLUME. ACTIONS WHICH COMPLEMENT THEIR HYPOTENSIVE EFFECTS IN BLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                                                                                                                                                                                                                                                                                                                              PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLT-UL996 (Rel. 34, Last sequence update)
AD DECT-2001 (Rel. 40, Last amontation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
ADM OR AM:
Sus scrofa PIP:
                                                                               TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN PHEOCHROMOCYTOMA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 VSVALMYLGSLAFLGADTARLDVASEFRKWNKWALSRGKRELRMSSSYPTGLADVKAGP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                  AMIDATION (G-42 PROVIDE AMIDE GROUP).
AMIDATION (G-147 PROVIDE AMIDE GROUP).
64C7D2A0B4654DFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                       Cleavage on pair of basic residues; Signal
                                                                                           ADRENAL MEDULLA. ALSO FOUND IN LUNG, VENTRICLE AND KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 185;
                                                                                                                                                                                                                                                                                                                                                                                               PREPROAM C-TERMINAL FRAGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                 SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 947; DB 1;
Pred. No. 7.7e-78;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 AA.
                                                                                                                                                                                                                                                                                                                                                                                   ADRENOMEDULLIN
                                                                                                                                                                                                                                                                                                      InterPro; IPR001710; Adrenomedullin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                    SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                     EMBL; S73906; AAC60642.1; -.
EMBL; D43639; BAA07756.1; ALT_SEQ.
PIR; JN0476; JN0476.
PIR; JN0684; JN0684.
PIR; JC2351; JC2351.
MIM; 103275; -
                                                                                                                                                                                                                                                                                                               Pfam; PF02039; Adrenomedullin; 1. PRINTS; PR00801; ADRENOMEDULN. Hormone; Amidation; Cleavage on pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.08; Fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                         20420 MW;
                                                                                                                                                                                                                            EMBL; D14874; BAA03589.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                          A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                       45
95
148
110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADML_PIG
P53366;
01-OCT-1996 (
01-OCT-1996 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||
FL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FL 182
                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                            PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                  PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                            PROPEP
                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                       PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADRENAL GLANDS, LUNG, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 AQIVIRPQDVKGSSRSPQASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                            TISSUE-Adrenal medulla;
MEDLINE-94139945; PubMed-8043068;
Kitamura K., Kangawa K., Kojima M., Ichiki Y., Matsuo H., Eto T.;
"Complete amino acid sequence of porcine adrenomedullin and cloning of CDNA encoding its precursor.";
FEBS Lett. 338:306-310(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP).
AMIDATION (G-147 PROVIDE AMIDE GROUP).
71/149460F5660A61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -! - FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 VPVALMYLGSLAFLGADTARLDVAAEFRKKWNKWALSRGKRELRLSSSYPTGIADLKAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ
Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 IYQFTDKDKDKVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
PRIWTS; PR00801; ADRENOMEDULN.
HORMOONE; AMIdation; Cleavage on pair of basic residues; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                           Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y., Kawamoto M., Minamino N., Matsuo H., Eto T.; "Identification and hypotensive activity of proadrenomedullin N-terminal 20 peptide (PAMP)."; FEBS Lett. 351:35-37(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.3%; Score 817; DB 1; Le
Larity 89:1%; Pred. No. 3.2e-66;
Conservative 10; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADRENOMEDULLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                           TISSUE-Adrenal medulla;
MEDLINE-94357274; PubMed-8076689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEAL_BOVIN STANDARD;
062827;
16-0CT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20893 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D14875; BAA03590.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41
92
146
188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 22-41.
                                                  NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22
45
95
153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KIDNEY
```

ö

```
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)]. Canis familiaris (Doq).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130
188 AA;
                                                                                                                                SEQUENCE FROM N.A.
                                                   NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                               45
95
148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146
                                                                                                                                                                                                                 AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADML_RAT
ID ADMI
AC P431
DT 01-N
DT 01-N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δy
                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADML_CANFA STANDARD; PRT; 188 AA.
077559; O9TVC9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
                                                                                                                                                                                                                                                                                                                                                                                                                       PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 VPVALMYLGSLAFLGVDTARLDVAAEFRKKWNKWALSRGKRELRESSSYPTGLADVKAGP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                           Barker S., Wood E., Clark A.J.L., Corder R.; "Cloning of bovine preproadrenomedulin and inhibition of its basal expression in vascular endothelial cells by staurosporine."; Life Sci. 62:1407-1415(1988).
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-2
                                                         Bos taurus (Bovine).
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMIDATION (G-147 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ001613; CAA04866.1; -.
InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; of basic residues; Signal.
Hormone; Amidation; Cleavage on pair of basic residues; Signal.
21 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVS-SKPQAHGAP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y SIMILARITY).
3002E79AB3B6612C CRC64;
                                                                                                                                                                                                                   CIRCULATION CONTROL (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 774.5; DB Pred. No. 2e-62; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY. ADRENOMEDULLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
                                                                                                                                      TISSUE=Aorta;
MEDLINE-98244567; PubMed=9585168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20981 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                92
146
188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 AA;
                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                     NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                     22
45
95
148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                           PEPTIDE
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                 ROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADML_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 924448
84448
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                      gene expression in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                 -! - FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMIDATION (G-147 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 VPVALLYLGSLAFLGADTARLDVASEFRKKWNKWAVSRGKRELRVSSSYPTGLAEVKAGP
                 Eukaryota; Metazoà; Ćhordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hormone; Amidation; Cleavage on pair of basic residues; Signal. SIGNAL 1 21 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADRENOMEDULLIN.
PREPROAM C-TERMINAL FRAGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Indels
                                                                                                                             SEQUENCE FROM N.A.
Indoto I., Jougasaki M.;
"Cloning of CDRA encoding canine adrenomedullin.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> K (IN REF. 2).
809D6A64F98F5578 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 771; DB 1;
; Pred. No. 4.2e-62;
10; Mismatches 14
                                                                                                                                                                                                                                                                                                                       Ono Y., Kojima M., Okada K., Kangawa K.;
"cDNa cloning of canine adrenomedullin and its
heart and blood vessels in endotoxin shock.";
Shock 10:243-247(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADML_RAT STANDARD; PRT; 185 AA P43145; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR001710; Adrenomedullin. Pfam; PF02039; Adrenomedullin; 1. PRINTS; PR00801; ADRENOMEDUIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                          MEDLINE-99002704; PubMed-9788655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF045773; AAD05423.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130
20929 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 86.1%
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U96127; AAD09957.1;
(Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41
92
146
188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115
41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146
```

ó;

マ

```
RESULT 6
                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                      MEDLINE=96102137; PubMed=8524787; White R.F., Clark R.K., Willette R.N., Wang X., Yue T.L., Barone F.C., White R.F., Feuerstein G.Z., Sulpizio A.C., Aiyar N.V., Ruffolo R.R. Jr., Feuerstein G.Z., Discovery of adrenomedullin in rat ischemic cortex and evidence for its role in exacerbating focal brain ischemic damage."; Proc. Natl. Acad. Sci. U.S.A. 93:11480-11484(1995).

- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASOBILATATOR
                                                                                                                                        MEDLINE-93384621; PubMed-7690563; Sakata J., Shimokuba T., Kitamura K., Nakamura S., Kangawa K., Amatsuo H., Eto T.; Matsuo H., Eto T.; Medeular cloning and biological activities of rat adrenomedullin, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
BY SIMILIARITY.
ADRENOMEDULLIN.
PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
              Proadrenomedullin N-20
 16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-2(
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMIDATION (G-144 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                        LUNG, KIDNEY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF02039; AULENCOMEDLIN.
PRINTS; PR00801; ADRENOMEDLIN.
Hormone; Amidation; Cleavage on pair of basic residues; Signal.
21 BY SIMILARITY.
21 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35CAD9A9DD19AE35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                     -1- TISSUE SPECIFICITY: EXPRESSED IN ADRENAL GLANDS, HEART, SPLEEN, DUODENUM AND SUBMANDIBULAR GLANDS.-1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32;
                                                                                                                                                                                                        ochem. Blophys. Res. Commun. 195:921-927(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.9%; Score 624.5; DB 172.0%; Pred. No. 5.1e-49;
Live 14; Mismatches 32
                                                                                                                             STRAIN-SPRAGUE-DAWLEY; TISSUE-Adrenal gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U15419; AAB60519.1; -.
InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
                                                                                                                                                                                                                                                                                                                                                            -1- SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20636 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D15069; BAA03665.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                     Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143
                                                                                                                                                                                             hypotensive peptide.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22
45
94
149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143
                                                                                                                                                                                                                                               TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Simi
Matches 126;
                                                                                                                                                                                                                                                                                                                                                AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEPTIDE
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROPEP
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
ADML_MOUSE STANDARD; PRT; 184 AA.
P97297; P97453;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last Annonamedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)],
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cells at the implantation site.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (G-145 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                           Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T., Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.; Genomic organization, expression, and chromosomal mapping of the mouse adrenomedullin gene"; Genomics 37:395-399(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
BY SINILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yotsumoto S., Ko M.S.H.; "Expression of mouse adrenomedullin gene in trophoblastic giant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cleavage on pair of basic residues; Signal. 21 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.2%; Score 570; DB 1; Length 184; 68.8%; Pred. No. 3.7e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C88C99045A79C898 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY. ADRENOMEDULLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> G (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:108058; Adm.
Interpro; IPR001710; Adrenomedullin.
Pfan: PF02039; Adrenomedullin; 1.
PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97092892; PubMed-8938454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20764 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D78349; BAA11367.1; -. EMBL; U77630; AAB36535.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92
144
184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41
                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hormone; Amidation; SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 119; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           FROM N.A.
                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22
45
95
151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
```

ä

121 IYQFTDKDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175

ö

윱

셤

ò

ð

음

```
DSSPDAARIRVKRYRQSMNNFQGLRSFG----CRFGT-CTV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94264012; PubMed-8204629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunol. 150:2992-3001(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochemistry 26:6508-6514(1987).
                                                                                                                                                  159 TLVSSKPQAHGAPAPPSGSAP 179
                                                                                                                                                                                  206 PSLSSSSFSPSSSPPPGDLP 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        internal repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                      LAHOIYO----
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Edgington T.S.;
                                                                                                                                                                                                                                                                FA5_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SULFATION
                                                                                    117
                                                  ద
                                                                                                                  g
                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ά
,
                                                61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                                             64 TOTLDPFLDEQNTTGPLQASNOSEAHIRVKRYRQSMN--QGSRSNGCRFGTCTFQKLAHQ 121
                    63
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDILNE-91288233; PubMed-2062660;
Taylor G.A., Lai W.S., Oakey R.J., Seldin M.F., Shows T.B.,
Eady R.L. T., Blackshear P.J.;
Eady R.L. T., Secured Sequence, alignment with related proteins,
and chromosomal localization of the mouse and human genes.;
Nucleic Acids Res. 19:3454-3454(1991).

I-FUNCTION: PROBABLE REGULATORY PROTEIN WITH A NOVEL ZINC FINGER
STRUCTURE INVOLVED IN REGULATORY PROTEIN WITH A NOVEL ZINC FINGER
HAS BEEN EXPERIMENTALY SHOWN TO BE ABLE TO BIND ZINC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----MKGASRSPE 78
01-A00-1992 (Rel. 23, Created)
01-A0G-1992 (Rel. 23, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Tristerraproline (TTP) (TISILA protein) (TISI) (ZFP-36) (Growth factor-inducible nuclear protein NUP475) (GO/GI switch regulatory
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclear protein; Repeat; Metal-binding; Zinc-finger; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61;
                                                                                                               121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAP 173
                                                                                                                                122 IYQLTDKDKDGMAPRNKISPQGYGRRRRRSLLEVLRSRTVESSQEQTHTAPAP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDD9AD950AF7AF98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Nuclear. INDUCTION: BY STIMULATION WITH VARIOUS MITOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: CONTAINS 2 C3H1-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 WALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 89.5; DB
Pred. No. 0.61;
                                                                                                                                                                                                                                 326 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C3H1-TYPE 1.
C3H1-TYPE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-P-P-G.
P-P-P-G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-P-P-G.
                                                                                                                                                                                                                                                                                                                                                           ZFP36 OR TIS11A OR TTP OR G0S24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 . C
34003 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000571; Zf-CCCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M92843; AAA58489.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M92844; AAC37600.1; -. EMBL; M63625; AAA61240.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00642; zf-CCCH; 2.
SMART; SM00356; ZnF_C3H1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45; Conservative
                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S34427; S34427.
MIM; 190700; -.
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198
219
109
147
                                                                                                                                                                                                                            TTP_HUMAN P26651;
                                                                                                                                                                                                                                                                                                                                               protein 24)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZN_FING
ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best
```

ò qq

```
"Posttranslational sulfation of factor V is required for efficient thrombin cleavage and activation and for full procoagulant activity."; Biochemistry 33:6952-6959(1994).
                                        146 LCHKFYLQGRCPYGSRCHFIHNPSEDLAAPGHPPVLRQSISFSGLPSGRRTSPPPPGLAG 205
-OK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-1600 FROM N.A.
MEDLINE=88107560; PubMed=2827731;
Rane W.H., Inthinose A., Hagen F.S., Davie E.W.;
"Cloning of cDNAs coding for the heavy chain region and connecting region of human factor V, a blood coagulation factor with four types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-87260886; PubMed-3110773;
Jenny R.J., Pittman D.D., Toole J.J., Kriz R.W., Aldape R.A.,
Hewick R.W., Kaufman R.J., Mann K.G.;
"Complete cDNA and derived amino acid sequence of human factor V.";
Proc. Natl. Acad. Sci. U.S.A. 84:4846-4850(1987).
                                                                                                                                                      ---FIDKDKDNVAP-----RSKISPOGYGRRRRSLPEAGPGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kane W.H., Davie E.W.;
"Cloning of a cDNA coding for human factor V, a blood coagulation factor homologous to factor VIII and ceruloplasmin.";
Proc. Natl. Acad. Sci. U.S.A. 83:6800-6804(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P12259, Q14285,
01-027-1989 (Rel. 12, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-027-2001 (Rel. 40, Last annotation update)
Coagulation factor V precursor (Activated protein C cofactor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Fibroblast;
MEDLINE=93203619; PubMed=8454869;
Shen N.L.L., Fan S.-T., Pyatl J., Graff R., Lapolla R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pittman D.D., Tomkinson K.N., Michnick D., Selighsohn U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-22232668; Pubmed=1567832;
Cripe L.D., Moore K.D., Kane W.H.;
"Structure of the gene for human coagulation factor V.";
Biochemistry 31:3777-3785(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The serine protease cofactor factor V is synthesized by lymphocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1188-1215 AND 1315-2224 FROM N.A. MEDLINE-86313665; PubMed-3092220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2224 AA
```

```
PDB; ICZS; 26-NOV-99.
PDB; ICZT; 26-NOV-99.
PDB; ICZV; 26-NOV-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                         MIM; 188055; -. MIM; 227310; -. MIM; 227400; -.
                                                                                                                                MIM; 134400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILAR
                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                             activated protein C.".
Nature 369:64-67(1994).
-I-FUNCTION: COAGULATION FACTOR V IS A COFACTOR THAT PARTICIPATES
WITH FACTOR XA TO ACTIVATE PROTHROMBIN TO THROMBIN.
-I-SUBUNIT: Factor Va is composed of a heavy chain and a light chain, noncovalently bound. The interaction between the two chains is calclum-dependent.
-I-DOMAIN: DOMAIN B CONTAINS 35 X 9 AA TANDEM REPEATS, AND 2 X 17 AA REPEATS.
                                                                                                                                                                                                                                                                                                                 PTM: Thrombin activates factor V proteolytically to the active cofactor, factor Va (formation of a heavy chain at the N-terminus and a light chain at the C-terminus).

PTM: SULEATION IS REQUIRED FOR EFFICIENT THROMEIN CLEAVAGE AND ACTIVATION AND FOR FULL PROCOAGULANT ACTIVITY.

DISEASE: OWNERN PARABEMOPHILLA, AN HEWORRHAGIC DIASTESIS, IS DUE TO A DEFICIENCY OF FACTOR V. OTHER DEFECTS IN FS RESULTS IN A FORM OF THROMBOPHILLA KNOWN AS APC RESISTANCE (APCR). THE APCR MUTATION IS FOUND IN ABOUT 5% OF THE POPULATION WHICH SUGGEST THAT IMPLANTATION.
                                                                                                                                                                       MEDLINE-94217810; Pubmed-8164741;
Bertina R.M., Koeleman B.P.C., Koster T., Rosendaal F.R.,
Dirven R.J., de Ronde H., van der Velden P.A., Reitsma P.H.;
"Mutation in blood coagulation factor V associated with resistance to
                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 3 F5/8 TYPE A DOMAINS; EACH IS COMPOSED OF PLASTOCYANIV-LIKE REPEATS.
SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
SIMILARITY: STRONG, TO COAGULATION FACTOR VIII.
                                                              X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 2065-2224.
MEDLINE-20052169; Pubmed-10586886;
Macedo-Ribeiro S., Bode W., Huber R., Quinn-Allen M.A., Kim S.W.,
Ortel T.L., Bourenkov G.P., Bartunik H.D., Stubbs M.T., Kane W.H.,
Fuentes-Prior P.;
                                                                                                                    'Crystal structures of the membrane-binding C2 domain of human
                               "Sulfation of tyrosine residues in coagulation factor V."; Blood 76:946-952(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOINED.
JOINED.
JOINED.
SULFATION.
MEDLINE-90366699; Pubmed-2168225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB59401.1;
AAB59401.1;
AAB59401.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L32779; AAB59401.1;
EMBL; L32755; AAB59401.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB59401.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB59401.1;
AAB59401.1;
                                                                                                                                         Nature 402:434-439(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB59401.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB59401.1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB59401.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB59401.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB59401.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB59401
                                                                                                                                                              VARIANT APCR GLN-534.
                                                                                                                               coagulation factor V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L32761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L32768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L32773;
                       Hortin G.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             + +
```

```
R InterPro; IPR001117; Cu-oxidase.

R InterPro; IPR001117; Cu-oxidase.

R InterPro; IPR00141; FA58_C.

R Pfam; PF001394; Cu-oxidase; 3.

R Pfam; PF001394; FE_RB_LYPe_C; 2.

R PROSTITE; PS001285; FA58C_1; 2.

R PROSTITE; PS01286; FA58C_2; 2.

R PROSTITE; PS01286; PS01286; PS01286; PS01286; PS01286; PS01286; PS01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TO 14 AA REPEATS IN BOVINE FAS.
35 X 9 AA APPROXIMATE TANDEM REPEATS OF
[TNP]-L-S-P-D-L-S-Q-T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X 17 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F5/8 TYPE A 1.
PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
F5/8 TYPE A 2.
PLASTOCYANIN-LIKE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 7
6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
Pred.
             JOINED.
JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.48;
EMBL, L32774, AAB59401.1; JC
EMBL, L32775, AAB59401.1; JG
EMBL, L32777, GAAB59401.1; JG
EMBL, L32777, AAB59401.1; JG
EMBL, L32778, AAB59401.1; JC
EMBL, M16967, AAB59401.1; JC
EMBL, M16967, AAB59532.1; --
PIR, A28827, A28897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11229
11238
112556
112656
112656
112663
11331
11331
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
1136
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
11336
113
```

-PTGVGFLHLAPGRLEELEPTQVS 243

450 AA.

١.

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
MEDLINB-92342131; PubMed-1353249;
Link R.E., Daunt D.A., Barsh G., Chruscinski A.J., Kobilka B.K.;
Link R.E., Daunt D.A., Barsh G., Chruscinski A.J., Kobilka B.K.;
Link R.E., Daunt D.A., Barsh G., Chruscinski A.J., Kobilka B.K.;
Storing of two mouse genes encoding alpha 2-adrenergic receptor
subtypes and identification of a single amino acid in the mouse alpha
2-C10 homolog responsible for an interspecies variation in
antagonist binding.";
                                                                                                                     125 TDKDKDNVAPRSKISPQGYGRRRRSLPEAG-----PGRTLVS-SKPQAHGAPA--- 172
                                                                                                                                                 MOI. Pharmacol. 42:16-27(1992).
-1- FUNCTION: ALPHA-2 ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
                                                 GASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGT-----CTVQKLAHQIYQF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                               244 WAYEPPEGSGPPAARDR-----FGSTPGLRRLECE-GTRDICPWLATPESIDFQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interlo,
Pfam; PF00001; 7tm_1; 1.
PRINTS: PR000237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; G-protein coupled receptor; Transmembrane; Glycoprotein; Multiqene family; Phosphorylation; Lipoprotein; Palmitat.
Multiqene family; Phosphorylation; Lipoprotein; Palmitat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:87934; Adra2a.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                            PRT;
FLDLDLSRIP-CDFYAGSGHKWLLA---
                                                                                                                                                                                                                                                                                                                                                            01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M99377; AAA37213.1; -.
                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1MMH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60
71
97
107
130
150
174
                                                                                                                                                                                                 173 PPSGSA 178
                                                                                                                                                                                                                                   340 PPGTDA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEINS.
                                                                                                                                                                                                                                                                                                                        A2AA_MOUSE
Q01338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCRDb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                              292
                                                    72
                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                   g
                                                    ŏλ
                                                                                                                            ò
                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=ARCC 27064 / DSM 738 / NRRL 3585;
MEDLINE-902099822; PubMed=1694525;
KOVACCEVIC S., Toblu M.B., Miller J.R.;
"The beta-lactam biosynthesis genes for isopenicillin N epimerase and deacetoxycephalosporin C synthetase are expressed from a single transcript in Streptomyces clavuligerus.";
J. Bacteriol. 172:3952-3958(1990).
                                                                                                                                               951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                       847 IRLLSLGAGEFKSQEHAKHKGPKVERDQAAKHRFSWMKLLAHKVGRHLSQDTGSPSGMRP 906
   Gaps
                                     3 VALMYLGSLAFLGADTAR-----LDVASEFRKKWNKWALSRGKRELRMSSSYPTGLAD 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATHWAY: BIOSYNTHESIS OF CEPHALOSPORIN ANTIBIOTICS. SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Actinobacteria, Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.NCBI_TaxID=1901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 216 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
397 AA; 43366 MW; A152741899F192FF CRC64;
                                                                                                           56 VKAGPAQTLIRPQDMKGASRSPED----SSPDAARIRVKRYRQSMNNFQGLRSFGCRFGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57;
   32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Purification and properties of isopenicillin N epimerase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.3%; Score 88.5; DB 1; Length 397; 24.7%; Pred. No. 0.94; tive 20; Mismatches 63; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces clavuligerus.";
Biochim. Biophys. Acta 999:78-85(1989).
--- FUNCTION: CATALYZES THE REVERSIBLE ISOMERIZATION BETWEEN
--- ISOPERICILLIN AND PERICILLIN N.
---- COFACTOR: PYRIDOXAL PHOSPHATE.
                                                                                                                                               907 WEDLPSODTGSPSRMRPWKDPPSDLLLLKQSNSSKILVGRWHLAS------
                                                                                                                                                                                 CTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYGRRRRSLPEAG-PGR 158
                                                                                                                                                                                                        InterPro; IPR000192; Aminotransi_class_v.
Pfam; PF00266; aminotran.5; 1.
PROSITE; PS00595; A.TRANSFER_CLASS_5; 1.
Antibiotic biosynthesis; Isomerase; Pyridoxal phosphate.
   Indels
   71;
                                                                                                                                                                                                                                                                                                                                             01-NOV-1990 (Rel. 16, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
1010-JUN-1994 (Rel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                            397 AA
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M32324; AAA26714.1; -.
InterPro; IPR000192; Aminotransf_class_V.
                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-23.
MEDLINE-90028393; PubMed-2804141;
   26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces clavuligerus
     Conservative
                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMINOTRANSFERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Usui S., Yu C.-A.;
                                                                                                                                                                                                                                                                                                            CEFD_STRCL
     39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                               CEFD_STRCL
                                                                                                                                                                                     112
                                                                                                                                                                                                                       952
       Matches
                                                                                                                                                                                                                                                                                                              g
                                                                         셤
                                                                                                             ð
                                                                                                                                                                                     ð
                                           ò
```

Ö

```
13 FLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQ-TLIRPQDMK 71
```

Palmitate.

```
entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                              PROSITE; PS01008; DNAA; 1.

DNA replication; DNA-binding; ATP-binding.

357 364

SEQUENCE 656 AA; 73182 MW; 6C1DSC01931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-NRK49F;
MEDLINE-94208523; PubMed-8156993;
                                                                        EMBL; AF187159; AAA26734.1; -. EMBL; AL357152; CAB92999.1; -.
                                                                                                                                      InterPro; IPR003593; AAA.
InterPro; IPR001957; Bac_DnaA.
                                                                                                                                                                                Pfam; PF00308; bac_dnaA; 1.
PRINTS; PR00051; DNAA.
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 25.4 les 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                       PIR; A41870; A41870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MPI2_RAT
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 DMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAH-QIYQFTDK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 EKKGAGGGOOPAEPSCKINDOKWYVIS-----SSIGSFFAPCLIMILVYVRIYQIA-K 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 DKDNVAPRSK----ISPQGYGRRRRRSL-PEAGPGRTLVSSKP---QAHGAPAPPSGSA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Calcutt M.J., Schmidt F.J.; "Conserved gene arrangement in the origin region of the Streptomyces coelicolor chromosome.";
                                                                                                                                                                                                                 SIMILARITY).
IMPLICATED IN CATECHOL AGONIST BINDING
                                                                                                                                                                                                                                                         (BY SIMILARITY).
IMPLICATED IN CATECHOL AGONIST BINDING
(BX SIMILARITY).
F07E225393AFA93B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces coelicolor.
Batchia, Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_raxID-1902;
                                                                           ('FUTENTIAL).

YETOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                 BY SIMILARITY.
PALMITATE (BY SIMILARITY).
IMPLICATED IN LIGAND BINDING (BY
                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                               54; Indels
                        6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
      CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 23, Last sequence update)
Chromosomal replication initiator protein dnaA.
BDNAA OR SCHIB.16C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          656 AA.
                                                                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 1.5; 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE DNAA FAMILY.
                                                                    7 (POTENTIAL)
CYTOPLASMIC (
                                                                                                                                                                                                                                                                                                                                                                     Score 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteriol. 174:3220-3226(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92250416; PubMed-1577691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNAA_STRCO STANDARD; PST902; Q9KXX4; O1-AUG-1992 (Rel. 23, Created) 01-AUG-1992 (Rel. 23, Last sand 16-OCT-2001 (Rel. 40, Last and
                                                                                                                                                                                                                                                                                                                       450 AA; 48865 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 51-656 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 28.9
  374
3399
409
450
10
10
14
188
1188
                                                                                                                                                                                                                                       200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
  218
375
400
410
431
10
10
144
113
                                                                                                                                                                                                                                   200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 P 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              285 P 285
                                                                                 DOMAIN
CARBOHYD
CARBOHYD
DISULFID
DOMAIN
TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                       LIPID
                                                                                                                                                                                             SILE
                                                                                                                                                                                                                                   SITE
                                                                                                                                                                                                                                                                             SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNAA_STRCO
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A PART OF THE PROPERTY OF THE PART OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                     74 SRSPEDSSPDAARIRVK-RYRQS--MNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKD 130
                                                                                                                                                                                                                                                                                                  95 PAGPAPQAPQSPPSRPQHRYEEPELPAPGGGGRE-------EYRDRDE- 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jinno S., Suto K., Nagata A., Igarashi M., Kanaoka Y., Nojima H., Okayama H.; Cac25a is a novel phosphatase functioning early in the cell cycle."; Cac25a is a novel phosphatase functioning early in the cell cycle."; In the call cycle. "; FUNCTION: THIS PROTEIN FUNCTIONS AS A DOSAGE-DEPENDENT INDUCER IN MITOTIC CONTROL. IT IS A TYROSINE PROTEIN PHOSPHATASE REQUIRED FOR PROGRESSION OF THE CELL CYCLE. IT MAY DIRECTLY DEPHOSPHORYLATE PROGRESSION OF THE CALL CYCLE. IT MAY DIRECTLY DEPHOSPHORYLATE PROGRESSION OF THE P34 (CDC2) KINASE ACTIVITY.
                                                                                                                                                          14 LGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGA 73
                                                                                                                        Gaps
                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tyrosine + phosphate.
-!- ENZYME REGULATION: STIMULATED BY CYCLINS B.
-!- SIMILARITY: STRONG, TO OTHER SPECIES M-PHASE INDUCER PHOSPHATASE
AND IN GENERAL TO PROTEIN-TYROSINE PHOSPHATASES.
                                                                                                                      46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
M-phase inducer phosphatase 2 (EC 3.1.3.48) (Dual specificity phosphatase Cdc2B).
                                                               9.2%; Score 87; DB 1; Length 656; 25.4%; Pred. No. 2.3; 1.1ve 16; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                131 NVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAP 179
                                                                                                                                                                                                                                                                                                                                                                                136 -----YEGYGRNRADQLPTARP-----AYPQEYQRPEPGSWPRP 169
rP (POTENTIAL).
6C1D5C0193D3C92B CRC64;
```

```
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.7%; Score 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No
                                                                                                                                                                               InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                                                       EMBL; M62372; AAA42034.1; -.
EMBL; U79031; AAC24959.1; -.
PIR; B40392; B40392.
PIR; JH0190; JH0190.
HSSP; P22274; JMMH.
GCRDb; GCR_0154; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48939 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158
253
264
305
333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333
445
450 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                   60
71
97
107
130
150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 P 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                               DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                     RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                         FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                           RANSMEM
                                                                                                                                                                                                                                                                                                RANSMEM
                                                                                                                                                                                                                                                                                                                                                               RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . م
                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                     OMAIN
                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an alpha 2-adrenergic
                                                                                                                                                                                                           106
                                                                                                                                                                                                                                114 PSPMDPQTAERTFEQALQAASRVIQKMQFTIKASVFASEAAGHSPVLQNITNSQALDSW- 172
                                                                                                                                                                                                                                                                   . Cell. Biochem. 144:181-190(1995).
FUNCTION: ALPHA-2 ADRENBRGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
                                                                                                                                                                             CRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISP-----QGYGRRRRSLPEAGPGRTL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wypijewski K., Duda T., Sharma R.K.;
"Structural, genetic and pharmacological identity of the rat alpha
2-adrenergic receptor subtype cA2-47 and its molecular
characterization in rat adrenal, adrenocortical carcinoma and bovine
                                                                                                                                                                 6 MYLGSLAFLGADTARLDVAS-EFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDUCED INHIBITION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lanier S.M., Downing S., Duzic E., Homcy C.J.; "Isolation of rat genomic clones encoding subtypes of the alpha 2-adrenergic receptor. Identification of a unique receptor subtype."; J. Biol. Chem. 266:10470-10478(1991).
                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1991 (Rel. 19, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2AAR)
                                                                                                                                                                                                           ----YROSMNNFOGLRSFG
                                                                                                                                            53;
                                                                                                                      8.8%; Score 83.5; DB 1; Length 574; 23.3%; Pred. No. 4; Live 23; Mismatches 79; Indels 53
                                                                                         BY SIMILARITY.
9367CE203B15FAAD CRC64;
                                          PRINTS: PRO015; MPIPHPHTASE.
PRINTS: PR00116; MPIPHPHTASE.
SMART; SM00450; RHOD; 1.
Cell division; Mitosis; Hydrolase; Multigene family.
ACT_SITE 481 481 BY SYMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chalberg S.C., Duda T., Rhine J.A., Sharma R.K.; "Molecular cloning, sequencing and expression of receptor complementary DNA from rat brain."; Mol. Cell. Blochem. 97:161-172(1990).
                                                                                                                                                                                                                                                                                                                                                                           450 AA.
                                                                                                                                                                                                            65 IRPQDMKGASRSPEDSSPDAARIRVKR-----
             HSSP; P30305; 1QB0.
InterPro; IPR000751; MPI_Phosphatase.
InterPro; IPR001763; Rhodanese_domain
                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-91125329; PubMed-2177834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-91244823; PubMed-1645350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-95349560; PubMed-7623790;
                                                                                                                                                                                                                                                                                                  161 VSSKPQAHGAPAPPSGSAPHFL 182
                                                                                                                                                                                                                                                                                                                     212 AEWASRREAFTORPS-SAPDLM 232
                                                                                                 574 AA; 64286 MW;
   EMBL; D16237; BAA03762.1;
                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
                                                                                                                                  l Similarity
47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEINS
                                                                                                                                                                                                                                                                                                                                                                           A2AA_RAT
P22909;
                                                                                       ACT_SITE
SEQUENCE
                                                                                                                         Query Match
                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADRA2A
                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                            173
                                                                                                                                                                                                                                                                                                                                                     RESULT 13
A2AA_RAT
                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                     g
    g
                                                                                                                                                                                                            ò
                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                  à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@illowing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 DKDNVAPRSK----ISPQGYGRRRRRSL-PEAGPGRTLVSSKP---QAHGAPAPPSGSA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 DMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAH-QIYQFTDK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        implicateD in Catechol agonist binding
(BY SIMILARITY).
P -> R (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMPLICATED IN CATECHOL AGONIST BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PALMITATE (BY SIMILARITY).
IMPLICATED IN LIGAND BINDING (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00237; GPCRRHODOPSN.
PR0SITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PR0SITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G_PROSITE; DS50262; G_PROTEIN_RECEP_F1_2; 1.
G_PROTEIN coupled receptor; Transmembrane; Glycoprotein;
Multigene family; Phosphorylation; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IVTVW -> HCHCV (IN REF. 2).
GL -> AV (IN REF. 1).
A -> G (IN REF. 2).
RP -> PR (IN REF. 1).
P -> R (IN REF. 1).
D -> N (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFA078DCA3D612AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
PALMITATE (BY
```

250 AA.

PRT;

STANDARD;

```
REPA_AGRTU
P15394;
q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 QGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG-RRRRSLPEAGPGR 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 SDTDNFP-------DSKDSPGDVQRSKLSPVLDGVSELRHSFDGSAADR 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 KRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Wataryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID-9606;
                                                                                                                                                                                                                                  MEDLINE-9534783; Pubmed-7619531; Bulfone A., Smiga S.M., Shimamura K., Peterson A., Puelles L., Rubenstein J.L.R.; A. Shimamura K., Peterson A., Puelles L., T. Drain-1: a homolog of Brachyury whose expression defines molecularly distinct domains within the cerebral cortex."; Neuron 15:63-78(1995).

- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN DEVELOPMENTAL PROCESSES. TBRI IS REQUIRED FOR NORMAL BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 682;
                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NAR-2002 (Rel. 41, Last annotation update)
T-brain-1 protein (T-box brain protein 1) (TBR-1) (TES-56).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01283; TBOX_1; 1.
PROSITE; PS01264; TBOX_2; 1.
PROSITE; PS50252; TBOX_3; 1.
Transcription regulation; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      573 POLY-ALA.
74053 MW; E1C8D84206EFBBB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                     -!- SUBGELEULE LOCATION: Nuclear (Potential).
-!- TISSUE SPECIFICITY: BRAIN.
-!- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
                                                682 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 8.5%; Score 80.5;
Best Local Similarity 23.9%; Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 TLVSSKPQAHGAPAPPSGSAPH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 YLLSQSSQPQSAATAPSAMFPY 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U49250; AAA92010.1; -. HSSP; P24781; 1XBR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P24781; 1XBR.
MIM; 604616; -
InterPro; IPR001699; T-box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34; Conservative
                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00907; T-box; 1. PRINTS; PR00937; TBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00425; TBOX; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   569 5
682 AA;
                                                                                                                                                                                                                         FISSUE-Fetal brain;
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                            TBR1_HUMAN
Q16650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA_BIND
                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

RESULT 15 REPA\_AGRIU

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 VKAGPAQTL-IRPQDMKG----ASRSPEDSSPDAARIR-----VKRYRQSMNNFQGLR 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYGRRRRS-----LPEAGPGR 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 E-----TVEDRIRABQLAGYVER----AAQNRPSGPRKAARRRQQSRCSFTTPNR-PRR 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 LMYLGSLAFLGADTARLDVA-SEFRKKWNKWALSRGKRELRMSSSY------PTGLAD 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 KORLPLEPAGARPRALLGKYVRKAAPLPD----DAAQARQERHDTIKAHMDSLSPADRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Minimal region necessary for autonomous replication of pTAR."; J. Bacteriol. 170:3170-3176(1988).
                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rhizoblaceae group; Rhizoblaceae; Rhizoblum. NCBL_TaxID=358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 27.2%; Pred. No. 3.2;
Matches 52; Conservative 24; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4A replication.
250 AA; 27987 MW; CCED106534831979 CRC64;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: October 17, 2002, 15:21:38
Job time : 11.4853 secs
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-88257036; PubMed-3290199; Gallie D.R., Kado C.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M21299; AAD15307.1; -.
                                                                                                                                                                  Agrobacterium tumefaciens
                                                                                                        Replicating protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLVSSKPQAHG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 TLPSSHPOKFG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A43662; A43662.
Plasmid; DNA replica
SEQUENCE 250 AA;
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COPY NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159
```

-1

```
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

using sw model protein search, OM protein October 17, 2002, 15:20:13 ; Search time 17.1922 Seconds (without alignments) 1017.222 Million cell updates/sec Run on:

US-10-018-924-2\_COPY\_4\_185

947 1 VSVALMYLGSLAFLGADTAR.....SKPQAHGAPAPPSGSAPHFL 182 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\* Database

pirl:\* pir2:\* pir3:\* pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		đ			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
1	947	100.0	185	,	JN0684	adrenomedulista
7	817	86.3	188		541600	
3	624.5	ഹ	185	~	JN0766	DI
4	95.5		1116		T16112	- 14
S	89.5	9.5	326		S34427	$\overline{}$
9	æ		2224		KFHUS	coaqulation factor
7	88.5	9.3	398		T52311	isopenicillin N ep
œ	87		450		149481	alpha-2 adrenergic
6	æ		656		A41870	dnaA protein - Str
10	83.5		260		T29586	Id
11	83.5		574		166868	
12	83	8.8	1051		C95367	conserved hypothet
13	82.5		450		JH0190	alpha-2-adrenergic
14	81.5	8.6	926		F88632	protein F56B3.4 [1
15	81	8.6			B40392	alpha-2-adrenergic
16	80	8.4			A43662	replicating protei
17	80	8.4	458		S24457	hypothetical prote
18	80		749		I37356	epithelial microtu
19	79		320		JC1255	TIS11 protein - ra
20	79		383		T39597	probable inositol
21	79	ж. Э.	450		A34169	alpha-2A-adrenergi
22	78.5		481		B43674	protein kinase (EC
23	78.5		1196		T14108	SH3-containing pro
24	78.5	8.3	1224		S28368	hypothetical prote
25	78.5		1796		S65004	probable membrane
26	78.5		2145		JC4747	adenylate cyclase
27	78		519		FOLJG4	gag polyprotein -
28	^		678		JC4245	transcription fact
53	77.5	8.5	199	~	T36622	hypothetical prote

hypothetical prote protein Y57G11C.9	hypothetical prote polynucleotide pho	hypothetical prote hypothetical prote	probable membrane	probable membrane parathyroid hormon	conserved hypothet	hypothetical prote	alpha-2-adrenergic	hypothetical Brach	hypothetical prote	transcription regu
T27245 H88904	T27246 AC1241	S70310 S59693	563325	S44203	T35971	T02286	A38316	178558	T21052	AG3448
0.0	7	0 0	2	7 (7	7 0	1 (1	7	N	~	01
553 568	659 723	1382	1859	591	860	327	450	681	2374	327
8.2	8 8	8 8	8.5	8.7	 	8.1.	8.1	8.1	8.1	8.0
77.5	77.5	77.5	77.5	77	77	76.5	76.5	76.5	76.5	92
30 31	32 33	34 35	36	38	39	41	42	43	44	45

## ALIGNMENTS

```
A/Gene: GDB.ADM
A/Cross-references: GDB:217070; OMIM:103275
A/Map position: 11pter-11qter
A/Introns: 33/2; 83/2
C/Keywords: amidated carboxyl end; blood pressure control; hormone
F/121/Domain: signal sequence #status predicted <PED>
F/12-11/Domain: proadrenomedullin #status predicted <PED>
F/12-11/Domain: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F/14-11/Domain: proadrenomedullin astatus experimental <MAT>
F/14-11/Domain: carboxyl-terminal propeptide #status predicted <PAP>
F/14-11/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F/14-11/Domain: carboxyl end (Arg) (amide in mature form from following F/110-115/Disulfide bonds: #status experimental
F/14-110-115/Disulfide carboxyl end (Tyr) (amide in mature form from following F/146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following F/146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following F/146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following F/146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following F/146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following F/146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following F/146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following F/146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following F/146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following F/146/Modified site: amidated carboxyl end (Tyr) (amide form from following F/146/Modified site: amidated carboxyl end (Tyr) (amide form from following form from following followi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: pheochromocytoma
R; Kitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.
Biochem. Biophys. Res. Commun. 194, 720-725, 1993
A;Title: Cloning and characterization of CDNA encoding a precursor for human adrenome A; Reference number: JN0684; MUID:93343928
A;Accession: JN0684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Rolecule type: protein
A; Residues: 22-41 <KI2>
R; Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto,
Biochem. Biophys. Res. Commun. 192, 553-560, 1993
A; Title: Adrenomeduliin: A novel hypotensive peptide isolated from human pheochromocy
A; Reference number: JN0476; MUID: 93249425
                                                                    C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #text_change 20-Jun-2000
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
C;Accession: JC2251; JN0684; PN0548; JN0476
R;Ishimitsu, T.; Kojima, M.; Kangawa, K.; Hino, J.; Matsuoka, H.; Kitamura, K.; Eto, Blochem Blophys. Res. Commun. 203, 531-639, 1994
A;Title: Genomic structure of human adrenomedullin gene.
A;Reference number: JC2351; MUID:94354869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-185 <ISH>
A;Cross-references: GB:S73906; NID:9765329; PIDN:AAC60642.1; PID:9765330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-185 <KIT>
A; Cross-references: GB:D14874; NID:g455470; PIDN:BAA03589.1; PID:g500612
A; Accession: PN0548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 95-146 <KI3>
A; Experimental source: pheochromocytoma
adrenomedullin precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: JN0476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: JC2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
```

ö

Gaps

; 0

Query Match
100.0%; Score 947; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 5.2e-80;
Matches 182; Conservative 0; Mismatches 0; Indels (

Length 185;

```
F:94-143/Product: adrenomedullin #status predicted <MAT>
F:41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following
F:143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following
                                                                                                                                                                                   Query Match 65.9%; Score 624.5; DB 2; Length Best Local Similarity 72.0%; Pred. No. 2.8e-50; Matches 126; Conservative 14; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.19
Best Local Similarity 22.29
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
S34427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adrenomedullin precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change ll-Jul-1997
R:Sakata, J: Shimokubo, T: Kitamura, K:; Nakamura, S:; Kangawa, K.; Matsuo, H.; Eto, T
Blochem. Blophys. Res. Commun. 195, 921-927, 1993
A:Anties moler and and biological activities of rat adrenomedullin, a hypotensiv A:Accession: JN0766
A:Accession: JN0766
A:Accession: JN0766
A:Accession: PN0610
A:Accession: PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reywords: amidated carboxyl end
1-21/Domain: signal sequence #status predicted <SIG>
122-185/Product: proadrenomedullin #status predicted <PEU>
12-41/Product: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  discontaining the first containing the first contai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                                                                                                                                                                                                          61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                                                                                                                                                                                                                                                                 121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAPH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||:|||||:||||| AQTVIRPQDVKGSSRSPQASIPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                 9
                                                                                         4 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 VPVALMYLGSLAFLGADTARLDVAAEFRKKWNKWALSRGKRELRLSSSYPTGIADLKAGP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:D14875; NID:g439721; PIDN:BAA03590.1; PID:g496379
                                                 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPKAGPGRTLVSSKPQAHGAPAPPS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.3%; Score 817; DB 2; Length 188;
89.1%; Pred. No. 5.1e-68;
ive 10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 89.1%
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adrenomedullin - pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||
FL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
S41600
                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                 ð
                                                                                                                                                                                                                                          ö
```

```
tristetraproline protein - human (C.Species: Homo sapiens (man) (C.Species: John-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999 (C.Species: John 1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999 (C.Species: John 1995 #sequence, R.J. Seldin, M.F.; Shows, T.B.; Eddy Jr., R.L.; Bl Nucleic Acids Res. 19, 3454, 1991 (M.C.) sequence, alignment with related proteins, and chromo A; Reference number: S34427; MUID:91288233 (A.Species) (M.S.) Sapiens (M.S.) Astatus: Preliminary A; Molecule type: mRNA A; Residues: 1-326 cqus (M.S.) (M.S.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: 218462
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-1116 <WUX>
A; Residues: 1-1116 <WUX
A; Resi
         ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F20D12.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16112
R;Wu, X.
Submitted to the EMBL Data Library, November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMNNFQG------LRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSK 137
Gaps
                                                                                                                                                                                                                                                            4 VSIALMILGSLAVLGADTARLDTSSQFRKKWNKWALSRGKRELQASSSYPTGLVDEKTVP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSSYP-TGLADVKA-----GPAQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQ 94
                                                                                                                                                                           1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 IYQFTDKDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37;
         'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.1%; Score 95.5; DB 2; Length 1116; 22.2%; Pred. No. 1.2; ive 26; Mismatches 63; Indels 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 I----SPQGYGRRRRSLPEAGPGRTLVSSKPQAHGAPAPP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 FGVTLAAPKGFGSISSLTEKPSSSIKSFGSWKPSSRSSPAPP 230
```

```
C;Goment: Factor V is activated by infomblin and partially by congulation factor ();Genetics:
A;Gene: GDB:155
A;Cross-references: GDB:119896; OMIN:227400
A;Nup position: 1q23-1q33
A;Introns: 53/2;84/1;125/1;196/1;244/1;318/1;373/2;432/3;466/1;537/3;588/1;
A;Introns: 53/2;84/1;125/1;196/1;244/1;318/1;373/2;432/3;466/1;537/3;588/1;
A;Pathway: blood coaquiation factor V; discoidin I amino-terminal homology; ferroxidase C;Reywords: blood coaquiation factor V stratus predicted cMATP
C;Reywords: blood coaquiation factor V stratus predicted cMATP
F;29-1274/Product: coaquiation factor V stratus predicted cMATP
F;29-34/Product: coaquiation factor V stratus predicted cMATP
F;29-34/Product: coaquiation factor V stratus predicted cMATP
F;39-35/Domain: ferroxidase repeat homology cF02>
F;39-40/Domain: ferroxidase repeat homology cF02>
F;39-137/Product: coaquiation factor Va light chain $status experimental cVAL>
F;39-137/Promain: B - CDB>
F;39-137/Domain: ferroxidase repeat homology cF03>
F;154-1305/Domain: discoidin I amino-terminal homology cDNI>
F;156-1224/Domain: discoidin I amino-terminal homology cDNI>
F;156-1224/Domain: discoidin I amino-terminal homology cDNI>
F;156-1234/Domain: discoidin I amino-terminal homology cDNI>
F;156-135/105-135/106-135/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-136/106-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isopenicillin N epimerase [validated] - Streptomyces clavuligerus
C;Species: Streptomyces clavuligerus
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C;Accession: 175211
R;Kovacevic, S.; Tobin, M.B.; Miller, J.R.
J. Bacteriol. 172, 3952-3958, 1990
A;Title: The beta-lactam biosynthetis genes for isopenicillin N epimerase and deaceto
Comment: Factor V is activated by thrombin and partially by coagulation factor Xa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 VKAGPAQTLIRPQDMKGASRSPED----SSPDAARIRVKRYRQSMNNFQGLRSFGCRFGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 VALMYLGSLAFLGADTAR-----LDVASEFRKKWNKWALSRGKRELRMSSSYPTGLAD 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 2224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 CTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAG-PGR 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---EKGSYEIIQ--DIDEDTAVNNWLISPQNASRAWGESTPLANKPGK 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 907 WEDLPSODTGSPSRMRPWKDPPSDLLLLKQSNSSKILVGRWHLAS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: T52311
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: M32324; PIDN: AAA26714.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.4%; Score 89; DB 23.2%; Pred. No. 10; tive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: Z26033; MUID:90299822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 23.2
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-398 <KOV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8;
                                                                                                                                                                                                                                         79 DSSPDAARIRVKRYRQSMNNFQGLRSFG----CRFGT-CTV------QK 116
                                                                                                                                                                                                                                                                                                                                                                          91 PTSPTATSTTPSRYKTEL----CRTFSESGRCRYGAKCOFAHGLGELRQANRHPKYKTE 145
                                                                                        Gaps
                                                                                                                                                                      -MKGASRSPE 78
                                                                                                                                                                                                                                                                                                                                               117 LAHQIYQ------FTDKDKDNVAP-----RSKISPQGYGRRRRSLPEAGPGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1188-1215,1315-2224 <KA2>
A; Cross-references: GB:M14335
A; Note: parts of this sequence were determined by protein sequencing
R; Keller, F.G.; Ortel, T.L.; Quinn-Allen, M.A.; Kane, W.H.
B; Chiler, F.G.; Trombin.catalyzed activation of recombinant human factor 'A; Reference number: A6139; MUID:95210278
A; Contents: annotation; thrombin cleavage sites
                                                                                        61;
                                        Length 326;
                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coagulation factor V precursor [validated] - human N;Alternate names: coagulation labile factor; proaccelerin
                                                                                        11;
                                Score 89.5; DB 2;
Pred. No. 1.1;
                                                                                        18; Mismatches
                                                                                                                                           34 WALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                159 TLVSSKPQAHGAPAPPSGSAP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 PSLSSSSFSPSSSPPPGDLP 226
                                     Query Match 9.5%;
Best Local Similarity 22.4%;
Matches 45; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
                                                                                                                                                                                              g
                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
```

5

Gaps

```
R;Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, May 1999
4; Reference number: 221575
A; Accession: T36566
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Mescule type: DNA
A; Mesidues: 1-82 < Coli>A; Residues: 1-82 < Coli>A; Residues: 1-82 < Coli>A; Cross-references: EMBL:AL049826; PIDN:CAB42692.1; GSPDB:GN00070; SCOEDB:SCH24.01c
A; Experimental source: strain A3(2)
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Genetics:
C; Genetics:
C; Genetics:
C; Genetics:
C; Genetics:
A; Genetics:
C; Genetics:
A; Genetics:
C; Genetics:
C; Genetics:
C; Genetics:
A; Genetics:
C; Genetics:
A; Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F55FB.4 - Caenorhabditis elegans
G:Species: caenorhabditis elegans
G:Species: Caenorhabditis elegans
G:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
G;Accession: T29586
A;Cession: T29586
A;Pescription: The Sequence of C. elegans cosmid F55FB.
A;Reference number: 220647
A;Recession: T29586
A;Accession: T29586
A;Accession: T29586
A;Accession: T29586
A;Accession: T29580
A;Residues: 1-560 < Car>
A;Residues: 1-560 < Car>
A;Residues: 1-560 < Car>
A;Residues: 1-50 < Car>
A;Cross-references: EMBL:UB0447; PIDN:AAB37808.1; GSPDB:GN00019; CESP:F55FB.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 PAGPAPQAPPSRPQHRYEEPELPAPGQGGRE-------EYRDRDE- 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRSPEDSSPDAARIRVK-RYRQS--MNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKD 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 LGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 DVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----VAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 9.2%; Score 87; DB 2; Length 656; Local Similarity 25.4%; Pred. No. 4; Head 43; Conservative 16; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 NVAPRSKISPQGYGRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    476 PLRRRQSSPMVASPRRRRSPSPERQRKRRSPSDSPPTRRLSTSPIRRRRSPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 PDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.8%; Score 83.5; Di
21.4%; Pred. No. 7.1;
tive 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 1
A; Introns: 56/2; 153/1; 320/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: CESP:F55F8.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
166868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cippecies: Mus musculus (house mouse)
Cippecies: Mus musculus (house mouse)
Cipate: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
Cibate: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
Cipate: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
Riths, R.; Daunt, D.; Barsh, G.S.; Chruscinski, A.; Kobilka, B.
Mol. Pharmacol. 42, 16-27, 1992
Antitle: Cloning of two mouse genes encoding alpha-2 adrenergic receptor subtypes and id a natagonist binding.
A.; Reference number: 149480; MUID:92342131
A.; Accession: 149481
A.; Status: preliminary; translated from GB/EMBL/DDBJ
A.; Molecule type: DNA
A.; Molecule type: DNA
A.; Molecule type: DNA
A.; Status: preliminary; translated from GB/EMBL/DDBJ
A.; Status: preliminary; translated from GB/EMBL/DDBJ
C.; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Keywords: neurotransmitter receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dnaA protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Accesaion: A41870; T35566
R;Calcutt, M.J.; Schmidt, F.J.
Bacteriol. 174, 3220-3226, 1992
A.Title: Conserved gene arrangement in the origin region of the Streptomyces coelicolor A;Reference number: A1870; MUID:92250416
A:Accesaion: A41870
A:Status: preliminary
A;Molecule type: DNA
A:Sesidues: 1-656 <CAL>
A;Cross-references: GB:M82836; NID:g6539740; PIDN:AAA26734.1; PID:g153240
                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                  198 FLDLDLSRIP-CDFYAGSGHKWLLA-------PTGVGFLHLAPGRLEELEPTQVS 244
                                                                                                                                                                                                                                                             72 GASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGT-----CTVQKLAHQIYQF 124
                                                                                                                                                                                                                                                                                                     125 TDKDKDNVAPRSKISPQGYGRRRRRSLPEAG-----PGRTLVS-SKPQAHGAPA--- 172
                                                                                                                                                                                                                                                                                                                                                                                                                       293 ------AELGP-GAIRARRELTDHARRLLADRPGRTLLTPDSPELSGGWAYRL 340
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 DKDNVAPRSK----ISPQGYGRRRRRSL-PEAGPGRTLVSSKP---QAHGAPAPPSGSA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 DMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAH-QIYQFTDK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKKGAGGGQOPAEPSCKINDQKWYVIS-----SSIGSFFAPCLIMILVYVRIYQIA-K 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 FLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQ-TLIRPQDMK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Gaps
                                                                                            57;
                                     Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 450;
                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54; Indels
                                                                                      63;
                                 ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
9.2%; Score 87; DB 2;
Best Local Similarity 28.9%; Pred. No. 2.7;
Matches 35; Conservative 14; Mismatches 5
         9.3%; Scc. 24.7%; Pred. No. 1...
                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (house mouse)
                                                                                      46; Conservative
                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341 PPGTDA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 PPSGSA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P 179
                           Query Match
                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
A41870
                                                                                                                                              à
                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
```

```
protein F56B3.4 [imported] - Caenorhabditis elegans
protein F56B3.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Dete: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: F88632
R;anonymous, The C: elegans Sequencing Consortium.
Sclence 282, 2012-2018, 1998
R;anonymous, The C: elegans Sequencing Consortium.
Sclence 282, 2012-2018, 1998
A;Atle: Genome sequence of the nematode C. elegans: a platform for investigating blo A;Atle: Genome sequence of the nematode C. elegans/ and www_sanger.ac.uk/Projects/C_A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A;Note: publishabed errata appeared in Sclence 283, 35, 1999; Science 283, 2103, 1999; A;Accession: PR8632
A;Atle Coule type: DMA
A;Molecule type: DMA
A;Molecule type: DMA
A;Molecule type: DMA
A;Molecule type: DMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GB:chr_IV; PIDN:AAC02615.1; PID:92854201; GSPDB:GN00022; CESP:F56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an alpha2-adrenergic recepto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is a predominant catecholamine receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dipha-2-adrenergic receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Bate: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Feb-1997
C;Accession: JH0190
R;Chalberg, S.C.; Duda, T.; Rhine, J.A.; Sharma, R.K.
Mol. Cell. Biochem. 97, 161-172, 1990
A;Title: Molecular cloning, sequencing and expression of an alpha2-adrenergian A;Reference number: JH0190; MUID:91125329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 ROSMNNFQGLRSFGCRFGTCTVQKLAH-QIYQFTDKDKDNVAPRSK-----ISPQGYGRR 146
310 FFRATAGKEPVRSEYRLRRADGSW-AWVIDVGQPRFSADGTFLGYVGSVLDITERRAAE- 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 KWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSSPDAARIRVKRY
                                                                                                                                                                          125 IDKDKDNVAPRSKISPQGYGRRRRSLPEAGPGRTL--VSSKP--QAHGAP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1450 < CHA>
A; Experimental source: brgin receptor is a predominant catech
C; Comment: Alpha source: brgin receptor is a predominant catech
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; transmembrane protein
F; 34 - 59/Domain: hydrophobic < HDI>
F; 71-96/Domain: hydrophobic < HII>
                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 RPNGLGPERGAGTAGGEAEPLPTQLNGAPGEPAPTRP 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 RRRSL-PEAGPGRTLVSSKP---QAHGAPAPPSGSAP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.7%; Score 82.5; Di
25.5%; Pred. No. 6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;106-13/Domain: hydrophobic <III>F;106-13/Domain: hydrophobic <HIV>F;150-175/Domain: hydrophobic <HIV>F;193-218/Domain: hydrophobic <HVP>F;375-400/Domain: hydrophobic <HVI>F;405-430/Domain: hydrophobic <VII>F;405-430/Domain: hydrophobic <VII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-926 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: JH0190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: F56B3.4
A;Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
                                                                                                                              65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                            gg
                                                                                                                                                                                                                                                                                                                                          δy
                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Status: preliminary
A:Molecule type: DNA
A:Molecu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Barnett, M.J; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows, Ralman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:D16237; NID:g484292; PIDN:BAA03762.1; PID:g1008042
C;Superfamily: human protein-tyrosine-phosphatase cdc25A; cdc25-type protein-tyrosine-ph
F;366-556/Domain: cdc25-type protein-tyrosine-phosphatase homology <PTP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein SMa1548 [imported] - Sinorhizobium meliloti (strain 1021) C; Species: Sinorhizobium meliloti C; Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001 C; Accession: C95367
                                                                                                                                                                                                                                       Ë
                                                                       Cispecies: Rattus sp. (rat)
Cispecies: Rattus sp. (rat)
Cispecies: Rattus sp. (rat)
Cispecies: Rattus sp. (rat)
Cispecies: Rattus sp. (sp. 48-1998 #sequence_revision 29-May-1998 #text_change 22-Jun-1999
Cispecies: Suto, R.; Nagata, A.; Igarashi, M.; Kanaoka, Y.; Nojima, H.; Okayama, EMBO J. 13, 1549-1556, 1994
A;Title: Cdc25A is a novel phosphatase functioning early in the cell cycle.
A;Reference number: IS3194; MuID:94208523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 CREGICIVQKLAHQIYQFIDKDKDNVAPRSKISP-----QGYGRRRRSLPEAGPGRIL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 ------EKDEAGYRAASSPGEDKENDGYIFKMPQKLPHSSSARAL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLGADTARLDVASEFRKK-----WNKWALSRGKRELRMSSS---YPTGLADVKAGPAQTL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 MYLGSLAFLGADTARLDVAS-EFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
8.8%; Score 83.5; DB 2; Length 574;
Best Local Similarity 23.3%; Pred. No. 7.3;
Matches 47; Conservative 23; Mismatches 79; Indels 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.8%; Score 83; DB 2;
26.9%; Pred. No. 16;
tive 18; Mismatches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 IRPQDMKGASRSPEDSSPDAARIRVKR-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEWASRREAFTORPS-SAPDLM 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 VSSKPQAHGAPAPPSGSAPHFL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: SMa1548
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
```

me

Ιţ

```
R.Lanler, S.M.; Downing, S.; Duzic, E.; Homcy, C.J.
J. Biol. Chem. 266, 10470-10478, 1991
J. Reference number: A40392; MUID:91244823
J. Reference number: A40392
J. Reference number: A40392
J. Residues: 1-450 < LAN>
J. Residues: 1-450 < LAN>
J. Residues: 1-450 < LAN>
J. Cross-references: GB:M62372; NID:9206615; PIDN:AAA42034.1; PID:9206616
C. Superfamily: Vertebrate rhodopsin
C. Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                              3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alpha-2-adrenergic receptor (clone RG10) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Dec.1991 #sequence_revision 03-Apr-1992 #text_change 13-Aug-1999
C;Accession: B40392
                                                                                                                                                                                                                                                                       PQ-DMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                        |: ||| |: || : | |: | |: || : | |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: |
                                                                                                                              Gaps
                                                                                                                                                                                           7 YLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIR 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 DMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAH-QIYQFTDK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 DKDNVAPRSK-----ISPQGYGRRRRRSLPEAGPGRTLVSSKP---QAHGAPAPPSGSA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 RRTRVPPSRRGPDACSAPPGGADRRPNAVGPERGAGTAGAEAFLPTQLNGAPGEPAPTR 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                              Length 926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57; Indels
                                                                                                                         Indels
Query Match 8.6%; Score 81.5; DB 2; I Best Local Similarity 24.0%; Pred. No. 19; Matches 29; Conservative 19; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

8.6%; Score 81; DB 2
Best Local Similarity 27.3%; Pred. No. 9.5;
Matches 33; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: October 17, 2002, 15:22:41 Job time : 18.1922 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 D 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 P 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 P 285
                                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  654
                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
Composition for promoting passive elongation of vesicle smooth muscle comprises adrenomedulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 26-27; 42pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-080754/09.
N-PSDB; AAF29138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted pro
UspA(1-57) - (A) - (GS
UspA(1-84) - (A) - (GS
UspA(1-56) - (DD) - (G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porcine adrenomedu
Porcine adrenomedu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat adrenomedulin
Rat adrenomedullin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human adrenomeduli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human adrenomedull
                                                                                                                                              October 17, 2002, 15:20:12; Search time 31.4202 Seconds (without alignments) 643.390 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Sinistry of the control of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                       1 VSVALMYLGSLAFLGADTAR....SKPQAHGAPAPPSGSAPHFL
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                   747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB60345
AAB60346
AAG00251
AAB75122
AAB75123
AAB75123
                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB49698
                                                                                                                                                                                                                                             US-10-018-924-2_COPY_4_185
947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB49697
                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1000.0
86.3
86.3
86.3
86.3
86.3
86.3
81.5
31.5
30.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            817
624.5
624.5
469
305.5
298
297.5
                                                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                               Seguence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                         ::
0
                                                                                                                                                                                                                                                          Title:
```

```
Adrenomedullin pep
Adrenomedullin pep
Adrenomedullin pep
Adrenomedullin pep
Adrenomedullin pep
Human preproadreno
Adrenomedullin pep
Human adrenomedullin pep
                                                                                                                                                                                                                                                                                                                                                                              Human Factor V. H
Human lipoprotein
Chimeric polyproli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagno
Murine leukaemia v
                                                                                                               Adrenomedullin pep
Rat adrenomedullin
                                                                                                                                                                                                                                                                                                                        Adrenomedullin pep
Adrenomedullin pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amphotrophic MLV r
Amphotrophic MLV r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human diagno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Envelope glycoprot
Murine leukemia vi
Murine leukemia vi
                                                       Human adrenomedull
Adrenomedullin pep
Human adrenomedull
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate can
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acremonium chrysog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polyproline beta-
                                   Thioredoxin-(GSGSG
                                                                                                                                                                                                                                                                                                                                                                Human TTP protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Passive elongation; vesicle smooth muscle; uropathic activity; adrenomedulin; urinary disorder; incontinence; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human adrenomedulin amino acid sequence.
                                                     AAB91759
AAE09818
AAB91763
AAB91763
AAE09819
                                                                                                                                               AAB91765
AAB91767
AAB91767
AAB91768
AAB91769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY26907
ABG05153
AAW44910
ABG19764
AAB75112
AAB75113
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2590
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR72590
AAY26901
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB63878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW26323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY26913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB19878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB19881
                                     AAB75114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB49697 standard; Protein; 185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUN-2000; 2000WO-JP04166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99JP-0177549
 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SHIO ) SHIONOGI & CO LTD
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
330.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
300.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200078338-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-DEC-2000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yanagita T;
                                                                                                                                                                                                                                                                                                                                                                                                                                        87.5
86.5
86.5
85
85
289
289
283
283
283
231
231
231
231
231
191.5
1063
107
107
107
                                                                                                                                                                                                                                                                                                                                                              89.5
                                                                                                                                                                                                                                                                                                                                                                                                                        88.5
                                                                                                                                                                                                                                                                                                                                                                                8
8
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB49697;
```

```
19
                                                                                                                                                                       64
                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                  184
                                                                                                                                                                                                                                                                                       AAB49698
                                                                                                                                                                                                                                                                              RESULT
   888888
                                                                                                                                                                       g
                                                                                                                 õ
                                                                                                                                  g
                                                                                                                                                     ò
                                                                                                                                                                                           ò
                                                                                                                                                                                                           g
                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                   ö
       This invention relates to a composition for promoting passive elongation of vesicle smooth muscle. The composition contains adrenomedulin, and has uropathic activity. The composition can be used for promoting passive elongation of vesicle smooth muscles, this is useful for releving uninary disorders such as impending urinary incontinence, reflex urinary incontinence and urinary incontinence with overflow. The present sequence composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composition for inhibiting automatic uterine contraction or contraction caused by bradykinin comprises adrenomedullin
                                                                                                                                                                                                                                                                                                                                                                                                            Human; adrenomedullin; precursor; bradykinin antagonist;
uterine contraction inhibitor; premature birth; miscarriage; abortion;
dysmenorrhoea; obstetric; gynaecological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a composition containing adrenomedullin for inhibiting automatic uterine contraction or contraction caused by bradykinin. The invention also relates to the use of adrenomedullin in
                                                                                                                                                                                        AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                                                                                                                                                                  IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPSGSAPH 180
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                     9
                                                                                                                                                            1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP
                                                                                                                                  ö
                                                                                                                 Length 185;
                                                                                                                                  Indels
                                                                                                             Score 947; DB 22;
Pred. No. 2.1e-93;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54pp; Japanese.
                                                                                                                                                                                                                                                                                                                                   AAB60344 standard; Protein; 185 AA.
                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                          Human adrenomedullin precursor.
                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JUN-1999; 99JP-0177548.
21-MAR-2000; 2000JP-0079171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JUN-2000; 2000WO-JP04167
                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                             Query Match
Best Local Similarity 100.
Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Page 37-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-080755/09.
                                                                                            185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAF27228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200078339-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo saplens
                                                                                                                                                                                                                                                                              ||
FL 185
                                                                                                                                                                                                                                                                                                                                                                        06-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-DEC-2000.
                                                                                                                                                                                                                                                                  FL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yanagita T;
                                                                                                                                                                                                                                                                                                                                                       AAB60344;
                                                                                            Sequence
                                                                                                                                                                                        61
                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                               124
                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                     184
                                                                                                                                                                                                                                                                                                                           AAB60344
                                                                                                                                                                                                                                                                                                                 RESULT
×88888888888888
                                                                                                                                                                    셤
                                                                                                                                                                                        ô
                                                                                                                                                                                                         g
                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                             õ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to a composition for promoting passive elongation of vesicle smooth muscle. The composition contains adrenomedulin, and has uropathic activity. The composition can be used for promoting passive elongation of vesicle smooth muscles, this is useful for relieving urinary disorders such as impending urinary incontinence, reflex urinary incontinence and urinary incontinence with overflow. The present sequence represents the porcine adrenomedulin protein, which is used in the composition of the invention.
the preparation of a drug for preventing premature birth or miscarriage. The composition of the invention can be used for preventing premature birth, preventing miscarriage, stopping delivery before caesarean section or for treating dysmenorrhoea. The present sequence represents human adrenomedullin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composition for promoting passive elongation of vesicle smooth muscle
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                  1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP
                                                                                                                                                                                                                                                                                                                                                                                   4 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Passive elongation; vesicle smooth muscle; uropathic activity; adrenomedulin; urinary disorder; incontinence; procine.
                                                                                                                                                                                                                                     Length 185;
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                               100.0%; Score 947; DB 22; 100.0%; Pred. No. 2.1e-93;
                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porcine adrenomedulin amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 31-33; 42pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB49698 standard; Protein; 188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUN-2000; 2000WO-JP04166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                         Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprises adrenomedulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-080754/09.
                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                            185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAF29139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200078338-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||
FL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yanagita T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa.
                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB49698;
                                                                                                                                                                                                                                     Query Match
```

123

63

Sequence Query Match

တ္ထ

Matches

8

g

à

g

õ

```
This invention relates to a composition for promoting passive elongation of vesicle smooth muscle. The composition contains adrenomedulin, and has uropathic activity. The composition can be used for promoting passive elongation of vesicle smooth muscles, this is useful for relieving urinary disorders such as impending urinary incontinence and urinary incontinence and urinary incontinence with overflow. The present sequence represents the porcine adrenomedulin rat, which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition for promoting passive elongation of vesicle smooth muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 VSIALMLIGSLAVLGADTARLDTSSQFRKKWNKWALSRGKRELQASSSYPTGLVDEKTVP
                                      AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ
                                                          VPVALMYLGSLAFLGADTARLDVAAEFRKKWNKWALSRGKRELRLSSSYPTGIADLKAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 IYQFTDKDKDNVAPRSKISPQGYGRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175
                                                                                                                IYQFTDKDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175
                                                                                                                                                                                                                                                                                                                                                                                                      Passive elongation; vesicle smooth muscle; uropathic activity; adrenomedulin; urinary disorder; incontinence; rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.9%; Score 624.5; DB 72.0%; Pred. No. 8e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 37-38; 42pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                    Rat adrenomedulin amino acid sequence
                                                                                                                                                                                                                                                      Æ
                                                                                                                                                                                                                                                    AAB49699 standard; Protein; 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUN-2000; 2000WO-JP04166.
                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comprises adrenomedulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-080754/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAF29140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200078338-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-JUN-1999;
                                                                                                                                                                                                                                                                                                                              04-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yanagita T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                          AAB49699;
                                                                          64
                                                                                                                  121
                                                                                                                                                                                                                                AAB49699
                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                  ŏ
                                                                        ద
                                                                                                                  ò
                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a composition containing adrenomedullin for inhibiting automatic uterine contraction or contraction caused by bradykinin. The invention also relates to the use of adrenomedullin in the preparation of a drug for preventing premature birth or miscarriage. The composition of the invention can be used for preventing premature birth, preventing miscarriage, stopping delivery before caesarean section or for treating dysmenorthosa. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition for inhibiting automatic uterine contraction or contraction caused by bradykinin comprises adrenomedullin \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porcine; pig; adrenomedullin; precursor; bradykinin antagonist; uterine contraction inhibitor; premature birth; miscarriage; abortion; dysmenorrhoea; obstetric; gynaecological.
                                                                                                                                                                                                                61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                                          Gaps
                                                                                                                9
                                                                                                                                    4 VPVALMYLGSLAFLGADTARLDVAAEFRKKWNKWALSRGKRELRLSSSYPTGIADLKAGP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
                                                                                                                1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP
                                                                                                                                                                                                                                                                    121 IYQFTDKDKDNVAPRSKISPQGYGRRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175
                                                                                                                                                                                                                                                                                        124 IYQFTDKDKDGVAPRSKISPQGYGRRRRRSLPEASLGRTLRSQEPQAHGAPASPA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                          ;
0
                                      Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.3%; Score 817; DB 22;
89.1%; Pred. No. 1.9e-79;
ive 10; Mismatches 9;
                                                                        6
                                      Score 817; DB 22;
Pred. No. 1.9e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        porcine adrenomedullin precursor
                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 43-44; 54pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                          Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porcine adrenomedullin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                        AAB60345 standard; Protein; 188
                                                                          10;
                                    86.3%;
89.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUN-1999; 99JP-0177548.
21-MAR-2000; 2000JP-0079171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-080755/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                      Similarity
Ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAF27229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200078339-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yanagita T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          represents
```

AAB60345;

AAB6034 RESULT

;;

Gaps

Length 185;

63

Sequence Query Match

Local

ò

AAB60346

```
Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer DNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 469; DB 21; Le
%; Pred. No. 1.6e-42;
                                                                                                                                                                                                                                                                                                                                                      Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 13; SEQ ID 4332; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.5%; Scor.
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UspA(1-57)-(A)-(GSGSGDAFE)-AM-gly protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYR 93
                  Human secreted protein, SEQ ID NO: 4332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB75122 standard; Protein; 120
                                                                                                                                                                                                                                  21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                         99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93; Conservative
                                                                                                                                                                                                                                                                                                                                                  Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-500381/45.
N-PSDB; AAC00257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 AA;
                                                                                                                                                                                                                                                                                                              (GEST ) GENSET
                                                                                                                  Homo sapiens
                                                                                                                                                       EP1033401-A2
                                                                                                                                                                                                                                                                       26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
Synthetic.
                                                                                                                                                                                           06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB75122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
AAB75122
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a composition containing adrenomedullin for inhibiting automatic uterine contraction or contraction caused by bradykinin. The invention also relates to the use of adrenomedullin in the preparation of a drug for preventing premature birth or miscarriage. The composition of the invention can be used for preventing premature birth, preventing miscarriage, stopping delivery before caesarean section or for treating dysmenorrhoea. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition for inhibiting automatic uterine contraction or contraction caused by bradykinin comprises adrenomedullin .
                                                                                                                                                                                                        Rat; adrenomedullin; precursor; bradykinin antagonist;
uterine contraction inhibitor; premature birth; miscarriage; abortion;
dysmenorrhoea; obstetric; gynaecological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VSVALMYLGSLAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IYQFTDKDKDNVAPRSKISPQGYGRRRRSLPEAGPGRTLVSSKPQAHGAPAPPS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   э;
Э
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.9%; Score 624.5; DB 72.0%; Pred. No. 8e-59; ive 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 48-49; 54pp; Japanese.
                                                   AAB60346 standard; Protein; 185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG00251 standard; Protein; 97
                                                                                                                                                                   Rat adrenomedullin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JUN-1999; 99JP-0177548.
21-MAR-2000; 2000JP-0079171.
                                                                                                                                                                                                                                                                                                                                                                                                       23-JUN-2000; 2000WO-JP04167.
                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-080755/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                       Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAF27230.
                                                                                                                                                                                                                                                                                                                            WO200078339-A1.
                                                                                                                            06-APR-2001
                                                                                                                                                                                                                                                                                                                                                                   28-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yanagita T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Sim
Watches 126;
                                                                                         AAB60346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG00251;
```

ö

Gaps

ö

Indels

06-OCT-2000 (first entry)

1

121

à 8

g

à

g

à

RESULT 7

AAG00251

axyxa

```
Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host.
                                                                                                                                                                                                                 producing the fused
                                                                                   Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host.
                                                                                                                                                                                          The present invention describes a method (M1) for producing adrenomedullin precursor. The method comprises: (a) producing the fuse protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SPDAARIRV 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                               Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
 ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 ELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDS----
Mitsushima
                                                                                                                                                                                                                                                                                                                                                                                                             31.5%; Score 298; DB 22;
57.4%; Pred. No. 6.1e-24;
tive 6; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UspA(1-56)-(DD)-(GSGSGDAFE)-AM-gly protein.
 Nakayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 17; Page 69-70; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                         Claim 17; Page 71; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB75123 standard; Protein; 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-2000; 2000WO-JP07023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99JP-0294147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitsuda Y,
 Mitsuda Y,
                                   WPI; 2001-282044/29.
N-PSDB; AAH19866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-282044/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                L Similarity
66; Conserv
                                                                                                                                                                                                                                                                                                                                                                          147 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAH19865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200127310-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-OCT-1999;
 rakimoto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takimoto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                               Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB75123;
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                         adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 ELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQG 101
                                                                                                                                                                                                                                                                                Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using recombinant host \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 DVNYSDLY-TGLIDVNLG------DMAGS-----GSGDAF----EYRQSMNNFQG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 120;
                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method (M1) for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 LRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG 144
                                                                                                                                                                                              Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .4e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 305.5; Dered. No. 7.4e-3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UspA(1-84)-(A)-(GSGSGDAFE)-AM-gly protein.
                                                                                                                                                                                              Nakayama T,
                                                                                                                                                                                                                                                                                                                                                   Claim 17; Page 68; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB75124 standard; Protein; 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.3%;
65.0%;
                                                                                   10-OCT-2000; 2000WO-JP07023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-0294147
                                                                                                                       99JP-0294147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-OCT-2000; 2000WO-JP07023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JUL-2001 (first entry)
                                                                                                                                                          (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67; Conservative
                                                                                                                                                                                          Takimoto A, Mitsuda Y,
                                                                                                                                                                                                                            WPI; 2001-282044/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 AA;
                                                                                                                                                                                                                                                N-PSDB; AAH19864
              WO200127310-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200127310-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                     15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-APR-2001
                                                  19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB75124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
```

a å g

ð

3;

Gaps

Length

```
31-JUL-2001
                                                                                                                                                                                                                                                                                                                                       19-APR-2001
                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                AAB75112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                 Best Local
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                 RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
                                                                                                                           AAB75112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB75113
                                                      à
                                                                            8
                                                                                                                                                    Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method (MI) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
The present invention describes a method (M1) for producing adrenomedulin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedulin precursor. The method can be used for the production of adrenomedulin precursor for pharmaccutical and diagnostic applications. AMH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host -
                                                                                                                                                                                                  42 ELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                  Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                          21; Gaps
                                                                                                                                                                                                                  DB 22; Length 120;
                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Glycine extended human adrenomedullin (AM-gly) protein.
                                                                                                                                                                                                                                                               102 LRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₹.
                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitsushima
                                                                                                                                                  Score 297.5; DB 2
Pred. No. 5.3e-24;
3; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 46; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                       Æ
                                                                                                                                                                                                                                                                                                                                    AAB75111 standard; Protein; 53
                                                                                                                                                   31.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2000; 2000WO-JP07023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99JP-0294147.
                                                                                                                                                               64.18;
                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitsuda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-282044/29
                                                                                                                                                  Query Match
Best Local Similarity
Matches 66; Conserv
                                                                                                                          120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAH19807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200127310-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takimoto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-APR-2001
                                                                                                                                                                                                                                                                                                                                                            AAB75111;
                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                        78
  888888888888888
                                                                                                                                                                                                  ð
                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                       셤
```

ś

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adrenomedulin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedulin precursor. The method can be used for the production of adrenomedulin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 repersent sequences which are used in the exemplification of the present invention.
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for pharmaceutical and diagnostic fused adrenomedullin precursor using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                        92 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDKDNVAPRSKISPQGYG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG 144
                                                                                                                                                1 YROSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a method (M1) for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitsushima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 30.5%; Score 289; DB 22; I Similarity 100.0%; Pred. No. 1.5e-23; 53; Conservative 0; Mismatches 0;
                Score 289; DB 22;
Pred. No. 1.5e-23;
                                                                       ö
30.5%; bcc. 100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycine extended adrenomedullin (AM-gly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takimoto A, Mitsuda Y, Nakayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 47; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Producing adrenomedullin useful application comprises producing recombinant host
                                                                                                                                                                                                                                                                                                            23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB75113 standard; Protein; 62
                                                                                                                                                                                                                                                                                                         AAB75112 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-OCT-2000; 2000WO-JP07023.
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SHIO ) SHIONOGI & CO LTD.
                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-282044/29
                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAH19808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200127310-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB75113;
```

⊼

```
The present invention describes a method (M1) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 repersent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host.
                                                                                                                                                                             for pharmaceutical and diagnostic
fused adrenomedullin precursor using a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 YROSMNNFOGLRSFGCRFGTCTVOKLAHQIYOFTDKDKDNVAPRSKISPQGYG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.5%; Score 289; DB 22; Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.8e-23;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitsushima
                                                                                       Mitsushima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 Similarity 100.0%; Pred. No. 6.8 53; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakayama T,
                                                                                       Nakayama T,
                                                                                                                                                                                                                                                      Claim 17; Page 49-50; 75pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 45; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human adrenomedullin (AM) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ¥.
                                                                                                                                                                             Producing adrenomedullin useful application comprises producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB75110 standard; Protein; 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-2000; 2000WO-JP07023.
                 99JP-0294147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SHIO ) SHIONOGI & CO LTD.
                                                     (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fakimoto A, Mitsuda Y,
                                                                                       Mitsuda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-282044/29.
                                                                                                                          2001-282044/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 AA;
                                                                                                                                                                                                                 recombinant host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAH19806
                                                                                                                          WPI; 2001-282044
N-PSDB; AAH19810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200127310-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-OCT-1999;
                 15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-APR-2001
                                                                                         Takimoto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB75110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a method (MI) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment, and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                               rroducing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                      Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGYG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 62;
                                  Linker peptide-adrenomedullin (AM) precursor protein.
                                                                                                                                                                                                                                                                                                                                                                 Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                 Mitsushima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 289; DB 22;
Pred. No. 1.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.5%; Scot. 100.0%; Pred. No. 1... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thioredoxin-(GSGSGDAFE)-AM-gly protein.
                                                                                                                                                                                                                                                                                                                                                                 Nakayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; Page 48; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB75114 standard; Protein; 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-2000; 2000WO-JP07023.
                                                                                                                                                                                                                                                                                        99JP-0294147.
                                                                                                                                                                                                                                                      10-OCT-2000; 2000WO-JP07023,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
31-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                            (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                               Fakimoto A, Mitsuda Y,
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-282044/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAH19809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200127310-A1.
                                                                                                                                                                             WO200127310-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens.
                                                                                                                          sapiens
                                                                                                                                                                                                                                                                                          15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-APR-2001
                                                                                                                                                                                                                 19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB75114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
```

Local

NAME OF THE PROPERTY OF THE PR

Matches

10

õ g RESULT 14 AAB75114 Ношо

ö

Gaps

; 0

Indels

꽃

```
ö
The present invention describes a method (MI) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                         Length 52;
                                                                                                                                                                                                                                                                     Query Match 29.9%; Score 283; DB 22; Length 52 Best Local Similarity 100.0%; Pred. No. 6.4e-23; Matches 52; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                52 AA;
                                                                                                                                                                                                                                Seguence
      88888888888
                                                                                                                                                                                                                                                                                                                                                              ò
```

Search completed: October 17, 2002, 15:21:13 Job time : 31.4202 secs

g

```
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

October 17, 2002, 15:20:12; Search time 6.51466 Seconds (without alignments) 742.931 Million cell updates/sec Run on:

US-10-018-924-2\_COPY\_22\_146 655 1 ARLDVASEFRKKWNKWALSR......FTDKDKDNVAPRSKISPQGY 125 Title: Perfect score: Sequence:

Scoring table:

105224 seqs, 38719550 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : , Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	HUMAN P35318 homo sapien	P53366 sus s	IN 062827 bos			P97297	P41593 mus	P25961	P02678	P12259	014215	P14480	007878		P07761		P4917	002793	085465	P49741 schizophy	P24634	P45816	004604	P07065	P30082	039504	P56869	7 chlar	P49454	P06565 baci	P02675 homo	HUMAN Q9p2g4 homo sapien
SUMM	ID	Ę	ADML_PIG	ADML_BO	ADML_CANFA	ADML_RAT	ADML_MOUSE	PTRR_MOUSE	PTRR_RAT	FIBB_PETMA	FA5_HUMAN	PRI1_SCHPO	FIBB_RAT	VP13_YEAST	MOXJ_METEX	SLS6_BRAOL	TBA_DICDI	GBB_MAIZE	SKI8_YEAST	GUN5_BACAG	TBAA_SCHCO	TBA2_EMENI	SC14_YARLI	TYRO_RANNI	TOP5_BPT4	GLR_RAT	EYA3_HUMAN	RPOB_CH	RPOB_CH	CENF_HU	GUN2_BACS4	FIBB_HU	YD83_HU
	DB	П											П	٦	Н	Н	7	Н	-	Н	-1												
	Length	185	188	188	188	185	184	591	591	477	2224	454	479	3144	300	436	457	380	397	400	448	451	497	532	442	485	573	1252	1252	3210	409	491	905
đ	Query Match	100.0	93.3	92.5	91.1	70.0	63.2	11.8	11.5	10.9	10.8	10.5	10.5	10.5	10.3	10.2	10.2	10.1	10.1	10.0					٠	•		•	٠	•	9.8	9.8	9.8
	Score	1	611	909	597	458.5	414	77	75	71.5	71	69	68.5	68.5	67.5	67	67	99	9	δ.	65.5	Š.	δ.	S.	65	65	65	65	65	ø	•	•	64.5
	Result No.		7	m	4	'n	ø	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32

Q01337 mus musculu P22086 rattus norv P47871 homo sapien P43811 haemophilus Q24546 drosophila P29713 anabaena sp Q08369 mus musculu P05432 rattus norv Q02020 gallus gall Q13389 saccharomyc P18439 mus musculu P184389 saccharomyc P18439	: 10
AZAC_MOUSE AZAC_RAT GELE HUMAN SPOT_HABIN SYN_DROME X457_ANASP G31A_MOUSE G31A_RAT FIBB_CHICK	VP3_ARMV
444 4458 6477 980 980 4460 995	360
$ \frac{1}{2} $	5.6
633 55 55 55 55 55 55 55 55 55 55 55 55 5	62.5
######################################	45

## ALIGNMENTS

```
SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                             PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
ADML_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142
       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
INHIBIT ALDOSTERONE SECRETION BY DIRECT ADRENAL ACTIONS. IN PRICITARY GLAND, BOTH PEPTIDES AT PHYSIOLOGICALLY RELEVANT DOSES INHIBIT BASAL ACTH SECRETION. BOTH PEPTIDES APPEAR TO ACT IN BRAIN AND PITUTTARY GLAND TO FACILITATE THE LOSS OF PLASMA VOLUME, ACTIONS WHICH COMPLEMENT THEIR HYPOTENSIVE EFFECTS IN BLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                               LEVELS FOUND IN PHEOCHROMOCYTOMA AND
                                                                                                                                                                                                                                                                                                                                                                  PROADRENCMEDULLIN N-20 TERMINAL PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                        AMIDATION (G-42 PROVIDE AMIDE GROUP).
AMIDATION (G-147 PROVIDE AMIDE GROUP).
64C7D2A0B4654DFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                            Cleavage on pair of basic residues; Signal.
                                                                -!- SUBCELLULAR LOCALLO...
-!- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN FILLY.
ADRENAL MEDULLA. ALSO FOUND IN LUNG, VENTRICLE AND KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                   PREPROAM C-TERMINAL FRAGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 655; DB 1;
Pred. No. 1e-61;
; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                       ADRENOMEDULLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 AA
                                                                                                                                                                                                                                                                                                       InterPro; IPR001710; Adrenomedullin. Pfam; PF02039; Adrenomedullin; 1. PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                           EMBL, D14874; BAA03589.1; -.
EMBL, S73906; AAC60642.1; -.
EMBL, D43639; BAA07756.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                             20420 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                           PIR; JN0476; JN0476.
PIR; JN0684; JN0684.
PIR; JC2351; JC2351.
MIM; 103275; -.
                                                                                                                                                                                                                                                                                                                                           Hormone; Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                             85 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADM OR AM.
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPQGY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPQGY 146
                                                       VESSELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADML_PIG
P53366;
                                                                                                                                                                                                                                                                                                                                                                                     PEPTIDE
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                           PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADRENAL GLANDS, LUNG, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
                                               Eto T.;
nd cloning
                                                                                                                                                                                                                                                 Kitamura K., Rangawa K., Ishiyama Y., Washimine H., Ichiki Y., Kawamoto M., Minamino N., Matsuo H., Eto T.; Identification and hypotensive activity of proadrenomedullin N-terminal 20 peptide (FAMP) "; FEBS Lett. 351:35-37(1994).
-1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP).
AMIDATION (G-147 PROVIDE AMIDE GROUP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 ARLDVAABERRKWHNKWALSRGKRELRLSSSYPTGIADLKAGPAQTVIRPQDVKGSSRSPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hormone, Amidation, Cleavage on pair of basic residues, Signal. SIGNAL _{
m 1}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PREPROAM C-TERMINAL FRAGMENT (BY SIMILARITY).
                                             Kitamura K., Kangawa K., Kojima M., Ichiki Y., Matsuo H., Et
"Complete amino acid sequence of porcine adrenomedullin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 611; DB 1; Length 18
Pred. No. 4.4e-57;
8; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71749460F5660A61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADRENOMEDULLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                       SEQUENCE OF 22-41.
TISSUE-Adrenal medulla;
MEDLINE-94357274; PubMed-8076689;
                  MEDLINE-94139945; PubMed-8043068;
                                                                                                  of cDNA encoding its precursor.";
FEBS Lett. 338:306-310(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20893 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D14875; BAA03590.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similario,
watches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
TISSUE-Adrenal medulla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
146
188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146
188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 SPQGY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                         AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADML_BOVIN
062827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROPEP
PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8844488
```

```
130 1
188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 113; Conserv
                    SEQUENCE FROM N.A
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                          22
45
95
148
                                                                                                                                                                                                                                                                                                                                                                                                                            146
                                                                                                                                                                                                                                                                                                                                                                                             110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 SPOGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 SPQGY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADML_RAT
P43145;
                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                            PEPTIDE
                                                                                                                                                                                                                                                                                                                                                               PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
                                                                                                                                                                                                                                                                                                                                                     PROPEP
                                                                                                                                                                                                                                                                                                                                                                          PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
ADML_RAT
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GE BALAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADML_CANFA STANDARD; PRT; 188 AA.
077559; OGTVC9;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
ADM Precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20 terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                             PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 ARLDVAAEFRKKWNKWALSRGKRELRESSSYPTGLADVKAGPVQTLIRPQDVKGASRSPQ 81
                                                                                                  AMIDATION (G-42 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
AMIDATION (G-147 PROVIDE AMIDE GROUP)
                              Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis
                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                           Cleavage on pair of basic residues; Signal. 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.5%; Score 606; DB 1; Length 188;
llarity 92.0%; Pred. No. 1.5e-56;
Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                              PREPROAM C-TERMINAL FRAGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    3002E79AB3B6612C CRC64;
                                                                                                                                                                                                                                                                                                                                                   ADRENOMEDULLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY)
                                                                                                                                                                                                                                                                         EMBL, AJ001613; CAA04866.1; -.
InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
Hormone; Amidation; Cleavage on pair
                                                                                         MEDLINE=98244567; PubMed=9585168;
                                                                                                                                                                                                                                                                                                                                                                                                                                     20981 MW;
                                                                                                                                                                                                                                                                                                                                41
92
146
188
                                                                                                                                                                                                                                                                                                                                                                                 115
                                                                                                                                                                                                                                                                                                                                                                                                                146
        taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                     188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
es 115; Conserv
                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              22
45
95
148
                                                                                                                                                                                                                                                                                                                                                                                 110
                                                                                                                                                                                                                                                                                                                                                                                                                146
                                               NCBI_TaxID=9913
                                                                                                                                                                                                                                                                                                                                                                                             41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 SPQGY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 SPQGY 146
                                                                               TISSUE=Aorta;
                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                   PEPTIDE
PROPEP
                                                                                                                                                                                                                                                                                                                               PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                          PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADML_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCSEEPTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilensib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=99002704; PubMed=9788655;
Ono Y., Kojima M., Okada K., Kangawa K.;
"CDNA cloning of canine adrenomedullin and its gene expression in the heart and blood vessels in endotoxin shock.";
Shock 10:243-247(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 ARLDVASEFRKKWNKWAVSRGKRELRVSSSYPTGLAEVRAGPAQTLIRTQDVKGASRNPQ 81
                                                                                                                                                                                                                                                                                                                 -! - FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (b) SIGNATION (G-147 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARÍTY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HORMONE; Amidation; Cleavage on pair of basic residues; Signal. SIGNAL 1 21 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.1%; Score 597; DB 1; Length 188; larity 90.4%; Pred. No. 1.3e-55; Conservative 6; Mismatches 6; Indels
                                                              Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> K (IN REF. 2).
809D6A64F98F5578 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
Imoto I., Jougasaki M.;
'Cloning of cDNA encoding canine adrenomedullin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY. ADRENOMEDULLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001710; Adrenomedullin. Pfam; PF02039; Adrenomedullin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF045773; AAD05423.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20929 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146
188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115
41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U96127; AAD09957
```

```
RESULT 6
ADML_MOUSE
                                    ò
                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                   STRAIN-SPRAGUE-DAWLEY; TISSUE-Adrenal gland;
MEDLINE-93384621; PubMed-7680563;
Sakata J., Shimokuba T., Kitamura K., Nakamura S., Kangawa K.,
Matsuo H., Eto T.;
"Molecular cloning and biological activities of rat adrenomedullin, a
                                                                                                                                                                                                White R.F., Clark R.K., Willette R.N., olo R.R. Jr., Feuerstein G.Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROADRENGMEDULLIN N-20 TERMINAL PEPTIDE.
S INVILLARITY.
ADRENOMEDULLIN.
PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                                                                                                              Wang X., Yue T.L., Barone F.C., White R.F., Clark R.K., Willette R.N. Sulpizio A.C., Aiyar N.V., Ruffolo R.R. Jr., Feuerstein G.Z.; "Discovery of adrenomedullin in rat ischemic cortex and evidence for its role in exacerbating food brain ischemic damage."; Proc. Natl. Acad. Sci. U.S.A. 92:11480-11484(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).

BY SIMILARITY.

AMIDATION (G-42 PROVIDE AMIDE GROUP)

(BY SIMILARITY).

AMIDATION (G-144 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                           -:- SUBCELLULAR LOCATION: Secreted.
-:- TISSUE SPECIFICITY: EXPRESSED IN ADRENAL GLANDS, LUNG, KIDNEY, HEART, SPLEEN, DUODENUM AND SUBMANDIBULIAR GLANDS.
-:- SIMILARITY: BELONGS TO THE ADRENOMEDULIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cleavage on pair of basic residues; Signal. 21 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N SIMILARITY).
35CAD9A9DD19AE35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                                                                                            hypotensive peptide.";
Biochem. Blophys. Res. Commun. 195:921-927(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.0%; Score 458.5; DB : 72.8%; Pred. No. 4.3e-41; ive 10; Mismatches 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001710; Adrenomedullin. Pfam; PF02039; Adrenomedullin; 1.
                                                                                                                                                                                    MEDLINE-96102137; PubMed-8524787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY
(Rat).
a; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00801; ADRENOMEDULN,
          Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 AA; 20636 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D15069; BAA03665.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U15419; AAB60519.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hormone; Amidation;
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
 norvegicus
                                                        SEQUENCE FROM N.A
                                  NCBI_TaxID-10116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22
45
94
149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPQGY 125
                                                                                                                                                                         TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91;
                                                                                                                                                                                                                                                                    AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ή
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQ 123
                   p97297; p97453;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor (Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAOTLIRPODMKGASRSPEDSS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yotsumoto S., Ko M.S.H.;

"Expression of mouse adrenomedullin gene in trophoblastic glant
cells at the implantation site.";

Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARÍTY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
AMIDATION (G-145 PROVIDE AMIDE GROUP)
AMIDATION (G-145 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                   Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T., Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.; Genomic organization, expression, and chromosomal mapping of the mouse adrenomedullin gene"; Genomics 37:395-399(1996).
                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cleavage on pair of basic residues; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C-TERMINAL FRAGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> G (IN REF. 2).
C88C99045A79C898 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2e-36;
184 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADRENOMEDULLIN
PREPROAM C-TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 414; DB
Pred. No. 2e-3
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:108058; Adm.
InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97092892; PubMed-8938454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20764 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D78349; BAA11367.1; -. EMBL; U77630; AAB36535.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.2%;
68.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144
184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144
                                                                                                                                                                                 musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hormone; Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 AA;
                                                                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22
45
95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144
                                                                                                                                                                                                                                                                                                                               STRAIN-129/SV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84;
ADML_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGENTS
                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25
                                                                                                                                                                                      Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

SPQGY 143

139

S

Ċ,

```
LD DDT ACCOOK NAME OF THE STATE OF THE STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the BWBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
STRAIN-BALB/C;
MEDLINE-9455468; PubMed-8197183;
MCCuajg K.A., Clarke J.C., White J.H.;
McCualg K.A., Clarke J.C., White J.H.;
Mcloeular cloning of the gene encoding the mouse parathyroid hormone/parathyroid hormone-related peptide receptor.";
Proc. Natl. Acad. Sci. U.S.A. 91:5051-5055(1994).
-I- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVITE ADENYLY.
CUCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                  PTRR_MOUSE STANDARD; PRT; 591 AA.
P41593; 062119;
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Parathyroid hormone/parathyroid hormone-related peptide receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-C3H/HEHA;
MEDLINE-95034305; PubMed-7524627;
Karperlan M., van Dijk T.B., Hoeijmakers T., Cremers F.,
Abou-Samra A.-B., Boonstra J., de Laat S.W., Defize L.H.K.;
Expression pattern of parathyroid hormone/parathyroid hormone
related peptide receptor mRNA in mouse postimplantation embryos
indicates involvement in multiple developmental processes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCRDb; GCR_1614; -.
MGD; MGI:97801; Pthr.
InterPro; IPR000832; GPCR_secretin.
InterPro; IPR001879; hormn_receptor.
Pfam; PF00002; 7tm_2; 1.
Pfam; PF02793; HRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L34611; AAA40011.1; -.
EMBL; L34608; AAA40011.1; JOINED.
EMBL; L34609; AAA40011.1; JOINED.
EMBL; L34610; AAA40011.1; JOINED.
EMBL; L34610; AAA40011.1; JOINED.
HSSP; Q03431; 1BL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            precursor (PTH/PTHR receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00249; GPCRSECRETIN. SMART; SM00008; HormR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X78936; CAA55536.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mech. Dev. 47:29-42(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCR_1005;
                                                                                                                                             ||
GY 144
                                                                                                   GY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCRDb;
                                                                                                                                                                                                                                                                                                             PTRR_MOUSE
                                                                                                   124
                                                                                                                                                                      143
                                                                                                                                                                                                                                                                         RESULT 7
                                                                                                   ŏ
                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                             DER NEUER PRESENTATION OF THE PRESENTATION OF
```

```
5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Bone;
MEDLINE-9212903; PubMed-1313566;
Abou-Samra A.-B., Jueppner H., Force T., Freeman M.W., Kong X.-F.,
Abou-Samra A.-B., Jueppner H., Bornentre J.V., Potts J.T. Jr.,
Schipani E., Urena P., Richards J., Bonventre J.V., Potts J.T. Jr.,
Kronenberg H.W., Segre G.V.;
"Expression cloning of a common receptor for parathyroid hormone and
parathyroid hormone-related peptide from rat osteoblast-like cells: a
single receptor stimulates intracellular accumulation of both cAMP
and inositol trisphosphates and increases intracellular free
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARATHYROID HORMONE/PARATHYROID HORMONE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 DVASEFRKKWNKWALSRG-KRELRM-SSSYP-----TGLADV--KAG---PAQTLIRP 49
                                                                                                                                                                                                                                                                                               4 (POTENTIAL).

EXPRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

MAISSING (IN REF. 2).
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-CTT-2001 (Rel. 40, Last annotation update)
Parathyroid hormone/parathyroid hormone-related peptide receptor precursor (PTH/PTHR receptor).
PTHR1 OR PTHR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.8%; Score 77; DB 1; Length 591; 32.5%; Pred. No. 1.6; Live 12; Mismatches 28; Indels
                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GA -> VS (IN REF. 2).
F7876F8D388BDDFD CRC64;
                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                           RELATED PEPTIDE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4).

AEF. 2).

1D388PT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 89:2732-2736(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISSING (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               591 AA
                                                                                                                                                                                   1 (POTENTIAL)
                                                                                                                                                                                                                                                             3 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66313 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | : | : | | | | 525 ATTNGHSQLPGHAKPGAPAI 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 QDMKGASRSPEDSSPDAARI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 32.58
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 591 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             283
307
3321
3321
3362
3362
3441
4441
1161
1166
1176
444
                                                                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTRR_RAT P25961;
                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                         TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                             RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                              FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                    DOMAIN
                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTRR_RAT
```

MEDLINE-94292182; Pubmed-8020952;

```
525 ATTNGHSQLPGHAKPGA 541
                                                                       FIBB_PETMA
                                                        RESULT 9
                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŝ
           Pausova Z., Bourdon J., Clayton D., Mattel M.-G., Seldin M.F., Janicka N., Stylere M., Szpirer G.; Janicka C.; Triviare M., Szpirer J., Levan G., Szpirer G.; Teceptor G. a parathyroid hormone-preparathyroid hormone-related peptide receptor (PTHR) cDNA from a rat osteosarcoma (UMR 106) cell line: chromosomal assignment of the gene in the human, mouse, and rat Genomics 20:20-26(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR ARATHYROID HORMONR-RELATED PEPTIDE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLY. CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARATHYROID HORMONE/PARATHYROID HORMONE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 DVASEFRKKWNKWALSRG-KRELRM-SSSYP-----TGLADV--KAG---PAQTLIRP 49
                                                                                                                                                                                         -i - SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS50227; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS50261; G_PROTEIN_RECEP_F2_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 75; DB 1; Length 591;
Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RELATED PEPTIDE RECEPTOR. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21944F3051B9E9C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .)
                                                                                                                                                                               -! - SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S (POTENTIAL CYTOPLASMIC 6 (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                       GCRDb; GCR_0938; ...
Interpro; FR000082; GPCR_secretin.
Interpro; IPR001879; horm_receptor.
Pfam; PF00002; 7tm_2; 1.
Pfam; PF02793; HRM; 1.
PRINTS; PR00249; GPCRECRETIN.
SMART; SM00009; HORMR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66260 MW;
                                                                                                                                                                                                                                                                                                                                  EMBL; M77184; AAA41811.1; -. EMBL; L19475; AAA68098.1; -. HSSP; Q03431; 1BL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.5%;
32.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDMKGASRSPEDSSPDA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         440
                                                                                                                                                                                                                                                                                                                                                                            GCRDb; GCR_0206; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          591 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 37-477 FROM N.A.

MEDLINE=87076582; PubMed=3790537;

MEDLINE=87076582; Doblittle R.E., Pontes M., Strong D.D.;

Bohonus V.L., Doolittle R.E., Pontes M., Strong D.D.;

"Complementary DNA sequence of lamprey fibrinogen beta chain.";

Blochemistry 25:6512-6516(1986).

-I. FUNCTION: FIBRINGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA AND GAMMA), LINKED TO BACH OTHER BY DISULLEDE BONDS.
-1- MISCELLANBOUS: CONVERSION OF FIBRINGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT IS CONVERTED INTO THE HARD CLOT BY FACTOR XILIA WHICH CATALYZES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
                                                                                                                                                                                                                                           Cottrell B.A., Doolittle R.F.; "Amino acid sequences of lamprey fibrinopeptides A and B and characterizations of the junctions split by lamprey and mammalian
                                                                                                              Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
                                                      01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY).
INTERCHAIN (WITH THE ALPHA CHAIN)
(BY SIMILARITY).
INTERCHAIN (WITH THE GAMMA CHAIN)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERCHAIN (WITH THE ALPHA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SIMILARITY: CONTAINS 1 FIBRINGEN C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A03124; A03124.

PIR; A25022; A25052.

INCECPIO; IPEZ.

INTERPIO; IPR002181; Fibrinogen_C.

Pfam; PF00147; fibrinogen_C; 1.

SMART; SM00186; FEG; 1.

PROSTIE: PS00514; FIBRIN AG_C_DOMAIN; 1.

Blood coagulation; Plasma; Sulfation; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIBRINOGEN BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SULFATION.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIBRINOPEPTIDE B.
 477 AA
                                                                                                                                                                                                                                                                                                                 Biochim. Biophys. Acta 453:426-438(1976).
                                                                                                                                                                                                                          MEDLINE-77065679; Pubmed-999898;
                                      21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M14773; AAA49261.1; -.
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36
37
477
13
27
84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66
                                                                                                                                                                                                         SEQUENCE OF 1-36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66
                                                                                                                                                                      NCBI_TaxID=7757
FIBB_PETMA P02678;
                                                                                                                                                                                                                                                                                                   chrombins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEPTIDE
NON_CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
```

```
7;
                                                                                                                                                                                                                             274 RVDGSSNFARDWNTYKAEFGNIAFGNGKSICNIPGEYWLGTKTVHQLTKQHTQQVLFDMS 333
                                                                                                                                                                                                                                                           51 DMKG-----ASRSPEDSSPDAARIRVKRYRQSMNN--FQGLRSFGCRFGTCTVQKLAH 101
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kane W.H., Ichinose A., Hagen F.S., Davie E.W.; "Cloning of cDNAs coding for the heavy chain region and connecting region of human factor V, a blood coagulation factor with four types
                                                                                                                                                                                                2 RLDVASEFRKKWNKW-----ALSRGKRELRMSSSYPTGLADV----KAGPAQTLIRPQ 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jenny R.J., Pittman D.D., Toole J.J., Kriz R.W., Aldape R.A., Mann K.G., Mann K.G., Monn K.G., "Complete cDNA and derived amino acid sequence of human factor V."; Proc. Natl. Acad. Sci. U.S.A. 84:4846-4850(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-86313665; PubMed-3092220;
Kane W.H., Davie E.W.;
"Cloning of a cDNA coding for human factor V, a blood coagulation
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                   27;
         (BY SIMILARITY).
INTERCHAIN (WITH THE GAMMA CHAIN)
(BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1989 (Rel. 12, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Coagulation factor V precursor (Activated protein C cofactor).
INTERCHAIN (WITH THE ALPHA CHAIN)
                                                                                                                                    Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Fibroblast;
MEDLINE=93203619; PubMed=8454869;
Shen N.L.L., Fan S.-T., Pyati J., Graff R., Lapolla R.J.,
                                                                                                                                                                 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92232668; PubMed-1567832;
Cripe LD., Moore K.D., Kane W.H.;
"Structure of the gene for human coagulation factor V.";
Blochemistry 31:3777-3785(1992).
                                                                                                      B8A95E7E32D09D18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor homologous to factor VIII and ceruloplasmin.";
Proc. Natl. Acad. Sci. U.S.A. 83:6800-6804(1986).
                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1188-1215 AND 1315-2224 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  2224 AA.
                                                                                                                                                 ; Pred. No. 4.9;
15; Mismatches
                                                                         SIMILARITY
                                                                                                                                    Score 71.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-87260886; Pubmed-3110773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-1600 FROM N.A. MEDLINE-88107560; Pubmed-2827731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochemistry 26:6508-6514(1987).
                                                                                                      54270 MW;
                                                                                                                                    10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      102 QIYQFT--DKDKDNVAP 116
                                                                                                                                                                                                                                                                                                                                                     389 NGMQFSTFDRDNDNWNP 405
                                                                                                                                                                   36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                        304
259
425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             internal repeats.
                                                        220
230
212
412 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                FAS_HUMAN
P12259; 014285;
01-0CT-1989 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Edgington T.S.;
                                                                        DISULFID
                            DISULFID
                                                                                                      SEQUENCE
DISULFID
                                                           DISULFID
                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                   g
SELETTE
                                                                                                                                                                                                                                                             ò
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- PTM: Thrombin activates factor V proteolytically to the active cofactor, factor Va (formation of a heavy chain at the N-terminus and a light chain at the C-terminus).

-:- PTM: SULFATION IS REQUIRED FOR EFFICIENT THROMBIN CLEAVAGE AND ACTIVATION AND FOR FULL PROCOAGUIANT ACTIVITY.

-:- DISEASE: OWREN PARAHEWOPHILIA, AN HEMORRHAGIC DIASTESIS, IS DUE TO A DEFICIENCY OF FACTOR V. OTHER DEFECTS IN FS REGULTS IN A FORM OF THROMBOPHILIA KNOWN AS APC RESISTANCE (APCR). THE APCR MUTATION IS FOUND IN ABOUT 5% OF THE POPULATION WHICH SUGGEST THAT A SILGHT THROMBOTIC TENDENCY MAY CONFER SOME ADVANTAGE IN FETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- FUNCTION: COAGULATION FACTOR V IS A COFACTOR THAT PARTICIPATES
-:- SUBDIVIT: FACTOR XA TO ACTIVATE PROTHROMBIN TO THROMBIN.
-:- SUBDIVIT: Factor Va is composed of a heavy chain and a light chain, noncovalently bound. The interaction between the two chains is calcium-dependent.
                                                                                                                                            "Posttranslational sulfation of factor V is required for efficient thrombin cleavage and activation and for full procoagulant activity."; Biochemistry 33:6952-6959(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ಧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- DOMAIN: DOMAIN B CONTAINS 35 X 9 AA TANDEM REPEATS, AND 2 X 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: CONTAINS 3 F5/8 TYPE A DOMAINS; EACH IS COMPOSED OF 2 PLASTOCYANIN-LIKE REPEATS.
-!- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
-!- SIMILARITY: STRONG, TO COAGULATION FACTOR VIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-94217810; PubMed-8164741;
Bertina R.M., Koeleman B.P.C., Koster T., Rosendaal F.R.,
Dirven R.J., de Ronde H., van der Velden P.A., Reitsma P.H.;
"Mutation in blood coagulation factor V associated with resistance
                                                                                                                                                                                                                                                                                                                                                                      Macedo-Ribeiro S., Bode W., Huber R., Quinn-Allen M.A., Kim S.W., Ortel T.L., Bourenkov G.P., Bartunik H.D., Stubbs M.T., Kane W.H., Fuentes-Prior P.,
                                                                                                                                                                                                                                                                                                                                                                                                                               "Crystal structures of the membrane-binding C2 domain of human
                                                                                                                                                                                                                                                                 Hortin G.L., "Sulfation of tyrosine residues in coagulation factor V.", Blood 76:946-952(1990).
                                                                                                             Pittman D.D., Tomkinson K.N., Michnick D., Selighsohn U.,
 ρλ
serine protease cofactor factor V is synthesized
                                                                                                                                                                                                                                                                                                                                         ANGSTROMS) OF 2065-2224.
                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (1.9 ANGSTRO)
MEDLINE=20052169; PubMed=10586886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                             MEDLINE-90366699; PubMed=2168225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB59401.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB59401.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOINED
                                                                                           MEDLINE=94264012; PubMed=8204629;
                                     Immunol. 150:2992-3001(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L32779; AAB59401.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB59401.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB59401.1;
AAB59401.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB59401.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB59401.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 402:434-439(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activated protein C.";
Nature 369:64-67(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT APCR GLN-534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      coagulation factor V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMPLANTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L32758;
L32759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L32760;
L32761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L32756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L32757;
                                                                                                                                    Kaufman R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEATS.
                         lymphocytes
                                                                            SULFATION
                                                                                                                                                                                                                              SULFATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
```

EMBL;

```
10.8%;
22.6%;
                                                                                                                                                  Local Similarity 22.6 ies 28; Conservative
      1346
1355
1354
1364
1382
1391
1400
1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                 1347
1356
1356
1374
1383
1392
1401
                                                                                                                                                                                                                                                                                              120 ISPQ 123
                                                                                                                                                                                                                                                                                                             1111
973 ISPQ 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
ACT_SITE
ACT_SITE
METAL
                                                                                                                                      Query Match
    REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                            REPEAT
                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                             RESULT 11
PRI1_SCHPO
      FILE
                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001117; Cu-oxidase.
InterPro; IPR000421; FA58_C.
InterPro; IPR000421; FA58_C.
InterPro; IPR000421; FA58_C.
SMART; SM00231; FS56_C; 2.
SMART; SM00231; FS56_C; 2.
PROSITE; PS01286; FA58_C.1; 2.
PROSITE; PS01286; FA58_C.1; 2.
Blood coagulation; Glycoprotein; Sulfation; Calcium; Signal; Zymogen; Repeat; Polymorphism; Disease mutation; Thrombophilia; 3D-structure.
SIGNAL
29 2224 COAGULATION FACTOR V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TO 14 AA REPEATS IN BOVINE FAS.
35 X 9 AA APPROXIMATE TANDEM REPEATS OF
[TNP]-L-S-P-D-L-S-Q-T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGION)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEAVY CHAIN.
ACTIVATION PEPTIDE (CONNECTING
LIGHT CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 x 17 AA TANDEM REPEATS.
1-1.
1-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F5/8 TYPE A 1.
PLASTCYANIN-LIKE 1.
PLASTCYANIN-LIKE 2.
F5/8 TYPE A 2.
PLASTCCYANIN-LIKE 3.
PLASTCCYANIN-LIKE 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-17.
22-13.
22-5.
22-10.
22-11.
22-113.
23-114.
  JOINED.
                                                                                                                                                                    Li. L32775; AAB59401.1; 07
Li. L32776; AAB59401.1; 07
Li. L32778; AAB59401.1; 07
Li. L32778; AAB59401.1; 07
Li. M16967; AAB59421.1; 07
Li. M16967; AAB59532.1; 07
Li. M25897; A25897.
                                                  AABS9401.1;
AABS9401.1;
AABS9401.1;
AABS9401.1;
AABS9401.1;
AABS9401.1;
                                                                                                                                             AAB59401.1;
AAB59401.1;
                                                                                                                                  AAB59401.1;
                           AAB59401.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2224
2224
3293
3293
329
329
684
684
684
684
928
928
928
928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11193
1202
1202
1211
1229
1229
1231
12319
1319
1318
1318
                                                                                                                                                                                                                                                                           1CZS; 26-NOV-99.
1CZT; 26-NOV-99.
1CZV; 26-NOV-99.
                                                                                                                                                                                                                                               PIR: A25897; A28
PDB; A28028; A2
PDB; ICZS; 26-W
PDB; ICZT; 26-W
PDB; ICZY; 26-W
MIM; 134400; --
MIM; 227310; --
MIM; 227310; --
MIM; 227400; --
                                                                                                                                                                                                                                                                                                                                               227310; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1135
                                                                                                                                           L32773;
L32774;
L32775;
L32776;
L32777;
                           L32764;
L32765;
L32766;
L32767;
L32767;
L32769;
L32770;
L32771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILAR
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
DOMAIN
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
```

```
3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                     62 --SSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSK 119
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 298531; CAB11078.1; -.
InterPro; IPR002755; DNA_primase_S.
Pfam; PF01896; DNA_primase_S; 1.
Transferase; DNA replication; DNA-directed RNA polymerase; Primosome.
ACT_SITE 66 66
                                                                                                                                                                                                            4 DVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPED-- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-972;
Gentles S., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;
Submitted (40G-1997) to the EMBL/Genbank/DDBU databases.
-!- FUNCTION: DNA PRIMARE IS THE POLYMERASE THAT SYNTHESIZES SMALL
RNA PRIMERS FOR THE OKAZAKI FRAGMENTS MADE DURING DISCONTINUOUS
DNA REPLICATION.
-!- SUBUNIT: HETERODIMER OF A SMALL SUBUNIT AND A LARGE SUBUNIT.
-!- SIMILARITY: BELONGS TO THE EUKARYOFIC PRIMASE SMALL SUBUNIT.
FAMILY.
                                                                                                                                                                                 24;
                                                                                                                                                   DB 1; Length 2224;
                                                                                                                                                 ; Score 71; DB 1; Length 222;
Pred. No. 30;
20; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
POTENTIAL.
71526FFAF7C2BBFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRII_SCHPO STANDARD; PRT; 454 AA. 014215; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1998 (Rel. 36, Last sequence update) Probable DNA primase small subunit (EC 2.7.7.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
POTENTIAL.
POTENTIAL.
2-18.
2-19.
2-20.
2-22.
2-23.
2-25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131
133
143
144
150
153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131
133
143
144
150
153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
SEQUENCE
```

```
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
VP13_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                     9
                                                                           -----QDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 102
                                                                                                                                       331 RLDVEVSRHLNHLLKSPFCVHPGTSRVCVPIDIERMDSFNPLK-----VPTVNDLLQE 383
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
                                                           4 DVASEFRKKW-----NKWA----LSRGKRELRMSSSYPTGLADVKAGPAQTLIRP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 183-479 FROM N.A.
MEDIATR=8937871; PubMed=2673932;
Eastman E.M., Gilula N.B.,
"Cloning and characterization of a cDNA for the B beta chain of rat
fibitinogen: evolutionary conservation of translated and
3'-untranalated sequences.";
Gene 79:151-158(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=WISTAR; TISSUE-Liver;
MEDLINE-87134033; PubMed=3817019;
Sobczak J., Lotti A.-M., Taroux P., Duguet M.;
"Molecular cloning of mRNA sequences transfently induced during rat
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95143386; PubMed-7841303; Courtney M.A., Bunce L.A., Neroni L.A., Simpson-Haidaris P.J.; Cloning of the complete coding sequence of rat fibrinogen B beta chain cDNA: interspecies conservation of fibrin beta 15-42 primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell Res. 169:47-56(1987).
FUNCTION: FIBRINGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                     36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-26 FROM N.A.
MEDLINE-84194000; PubMed-6232608;
Fowlkes D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;
Fortential basis for regulation of the coordinately expressed fibrinogen genes: homology in the 5' flanking regions.";
Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).
                                                                                                                                                                                                                                                                               01-JAN-1990 (Rel. 13, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
01-CCT-1902 (Rel. 41, Last annotation update)
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
          DB 1; Length 454;
                                   43; Indels
                                                                                                                                                                                                                                                        479 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 19-32.
Blomback B., Blomback M., Grondahl N.J.;
Bludies on fibrinopeptides from mammals.";
Acta Chem. Scand. 19:1789-1791(1965).
                        Pred. No. 8.4;
      10.5%; Score 69; DB 24.4%; Pred. No. 8.4; ive 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             structure.";
Blood Coagul. Fibrinolysis 5:487-496(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver;
                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 425-479 FROM N.A.
                                  32; Conservative
                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                103 IYQFTDKDKDN 113
                                                                                                                                                                                 384 L----DKNSQN 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     liver regeneration."
Exp. Cell Res. 169:4
                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGREGATION.
         Query Match
                                                                                                                                                                                                                                                         FIBB_RAT
                                                                                                               20
                                  Matches
                                                                                                                                                                                                                               RESULT
                                                                                   g
                                                                                                                                                                                         q
                                                                                                               ð
                                                                                                                                       d
                                                                                                                                                                 ŏ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. SIMILARITY: CONTAINS I FIBRINOGEN C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 RQDGSVDFGRKWDPYKKGFGNIATNEDTKKYCGLPGEYWLGNDKISQLTRIGPTELLIEM 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 QDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFG-----TCTVQKLA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :| || : : | : | : | : | : | : | | : | | : | | : | | : | | | : | | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 RLDVASEFRKKWNKWALSRG-----KRELRMSSSYPTGLADV----KAGPAQTLIRP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 BY SIMILARITY.
258 BY SIMILARITY.
425 BY SIMILARITY.
382 N-LINKED (GLCNAC. ..) (POTENTIAL).
30 LSI -> ILS (IN REF. 3).
439 L -> Q (IN REF. 5).
441 S -> T (IN REF. 5).
445 S -> A (IN REF. 5).
445 S -> A (IN REF. 5).
457 N -> F (IN REF. 5).
458 N-> F (IN REF. 5).
467 R -> F (IN REF. 5).
478 V -> F (IN REF. 5).
479 V -> F (IN REF. 5).
475 V -> F (IN REF. 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VP13_YEAST STANDARD; PRT; 3144 AA.
VP13_YEAST 000040;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation vpdate)
VPS13 OR SOII OR YLLO40c.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIBRINOPEPTIDE B.
INTERCHAIN (WITH THE ALPHA CHAIN)
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 68.5; DB 1; Length 479;
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U05675; AAA64666.1; --
EMBL; M27220; AAA41160.1; --
EMBL; K01336; AAA44159.1; --
EMBL; M5629; A65299;
PIR; A65299; A65299.
PIR; PE0010; PE0010.
HSSP; PC0675; IFEC.
InterPro; IPR002181; Fibrinogen_C.
Pfam; PF00147; fibrinogen_C:
Pfam; PF00147; Fibrinogen_C:
Pfam; PF00147; Fibrinogen_C:
NART; SM00186; FEG; 1.
SMART; SM0186; FIBRIN_AG_C_DOMAIN; 1.
Blood coagulation; Plasma; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIBRINGEN BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | : |:|| : | : | 388 HNGMFFSTYDRDNDGWVTTDPRKQCSKE 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 HQIYQFTDKDKDN-----VAPRSKISPQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18
479
32
211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     475
479 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERRATUM.
Nasrallah J.B., Kao T.-H., Goldberg M.L., Nasrallah M.E.;
Nature 326:523-523(1987).
Nature 326:523-523(1987).

-!- FUNCTION: INVOLVED IN SPOROPHYTIC SELF-INCOMPATIBILITY SYSTEM
(THE INABILITY OF FLOWERING PLANTS TO ACHIEVE SELF-FERTILIZATION).
-!- POLYMORPHISM: THERE ARE A TOTAL OF 50 DIFFERENT S ALLELES IN
B.OLERACEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nasrallah J.B., Kao T.-H., Chen C.H., Goldberg M.L., Nasrallah M.E.; "Amino-acid sequence of glycoproteins encoded by three alleles of the S. locus of Brassica oleracea."; S. locus of Brassica oleracea."; Nature 326:617-619(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nasrallah J.B., Kao T.-H., Goldberg M.L., Nasrallah M.E.; "A cDNA clone encoding an S-locus-specific glycoprotein from Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudloctyledons; core eudlocts; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID=3712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 ALSRGKRELRMS----SSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSSPDAARIRVK 72
extorquens AM1 moxF and
              Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               36; Indels
                                                                                                                                                                                                                                                                                                                                                          1 25 POTENTIAL.
26 300 MOXJ PROTEIN.
300 AA; 32425 MW; BC347551D51B542F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-A0G-1988 (Rel. 08, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
S-locus-specific glycoprotein S6 precursor (SLSG-6).
                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
"Nucleotide sequence of the Methylobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                              10.3%; Score 67.5; Di
30.1%; Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Mismatches
                                                                                                                                                                                                                                                                                           PIR; JQ0707; JQ0707.
InterPro; IPR001638; SBP_bac_3.
SMART; SM00062; PBPb; 1.
Signal; Methanol utilization; Periplasmic.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 RYRQ---SMNNFQGLRSFGCRFGTCTVQKLAHQ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAEQPPLSMKDGSGLEN---RIATTVAEAMGRK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brassica oleracea (Cauliflower).
                                                                                                                                                                                                                                                                           EMBL; M31108; AAA25381.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 22-435 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 318:263-267(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 28; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLS6_BRAOL
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                       Luo W., Chang A.;
Unpublished observations (XXX-1997).

-I- FUNCTION: PROMOTES ENDOSOWAL CYCLING OF TGN MEMBRANE PROTEINS BY
MODULATING THE FUNCTION OF TWO CYTOSOLIC TGN LOCALIZATION SIGNALS.

-I- SIMILARITY: SOME, TO S.POMBE SPBC16C6.02C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1354 SGGKGEIKSPSPDPASL----SSESERTATPQSLQGSNKSNIKNPEQKYLDFSFKAPKIA 1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 VKRYRQ-----SMNN------FQGLRSFGCRFG---TCTVQXLAHQIYQFTDKD----K 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRS----PE----DSSPDAARIR 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STAIN-AMI / NCIB
MEDLINE-90337342; Pubmed-2116368;
Anderson D.J., Morris C.J., Nunn D.N., Anthony C., Lidstrom M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Methylobacterium group; Methylobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3144;
                                                                                                                                    SEQUENCE OF 1-1360 FROM N.A.
Duesterhoeft A., Floeth M., Heuss-Neitzel D., Hilbert H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3144 AA; 357843 MW; BEE9B55BA2AD515B CRC64;
                                                                                   Brickner J.H., Fuller R.S.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                         Wedler H., Wedler E., Scharfe M., Wambutt R.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                        Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
 Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 14, Last sequence update) (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 68.5; DB
Pred. No. 82;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.5%; Scc.
28.0%; Pred
                                                                                                                                                                                                                       SEQUENCE OF 1095-3144 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF001317; AAC08284.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1990 (Rel. 14, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 273144; CAA97490.1; -. EMBL; 273145; CAA97491.1; -. SGD; SO003963; VPS13. SEQUENCE 3144 AA; 357843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methylobacterium extorquens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MoxJ protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1466 DNKHTELIPKSK 1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 DN----VAPRSK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           CHARACTERIZATION
                 NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=408;
                                                                   STRAIN-S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOXJ_METEX
P16028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOXJ_METEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

Š,

Gaps

15;

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 RPQDMK-----GASRSPEDSSPDAARIRVKRYRQSMNNF---QGL----RS---FGCR 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RLDVASEFRKKWNKWALSRGKRELRMSSS------YPTG--LADVKAGPAQTLI 47
                                                                                                                                                                                                                                                                                     (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
-!- SIMILARITY: TO THE EXTRACELLULAR PORTION OF A MAIZE PROTEIN KINASE RECEPTOR (ZMPK1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                :09
                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                   10.2%; Score 67; DB 1; Length 436; 25.3%; Pred. No. 13; tive 22; Mismatches 42; Indels
                                                                                                                                                                                                                                                                          Glycoprotein; Polymorphism; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 FSGIPEDQKLSYMVYNFTENSEEVAYTFRMTNNSIYSRLTLSSEGY 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 F-GTCTVQKLAHQIYQFTDKDKD------NVAPRSKISPQGY 125
                                                                                                                                       EMBL; Y00268; CAA68375.1; -.
EMBL; X03170; CAA56934.1; ALT_INIT.
PIR; A27827; A27827.
InterPro; IPR001480; B_lectin.
InterPro; IPR001869; Pan_app.
InterPro; IPR001869; Slocus_glycop.
Fam; PF001453; Agglutinin; 1.
Pfam; PF001453; Agglutinin; 1.
SMART; SM00108; B_lectin; 1.
SMART; SM00473; PAN_AP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               42; Conservative
                                                                                                                                                                                                                                                                                      436
436
46
64
114
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           436 AA;
                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
```

Search completed: October 17, 2002, 15:21:36 Job time: 7.51466 secs

THIS PAGE BLANK (USPTO)

```
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

- protein search, using sw model OM protein

Run on:

October 17, 2002, 15:20:13 ; Search time 11.8078 Seconds (without alignments) 1017.222 Million cell updates/sec

US-10-018-924-2\_COPY\_22\_146

655 1 ARLDVASEFRKKWNKWALSR......FTDKDKDNVAPRSKISPQGY 125 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

PIR\_71:\* Database :

pir1:\* pir2:\* pir3:\* pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	adrenomedullin pre	adrenomedullin - p	adrenomedullin pre	parathyroid hormon		parathyroid hormon	conserved hypothet	fibrinogen beta ch	. coaqulation factor		Æ	fibrinogen beta ch	protein F56B3.4 [i	hypothetical prote	VPS13 protein - ye	hypothetical prote	rod shape-determin	probable phospholi	methanol oxidation	S-locus-specific q	141K protein - pea	GTP-binding protei	antiviral protein	ARHGAP9 protein -			tubulin alpha-2 ch	phosphatidylinosit	monophenol monooxy
SUMMARIES	DI	JN0684	S41600	JN0766	S44203	159297	154195	C95367	A25052	KFHU5	T08036	T39017	A05299	F88632	H86389	S64791	T28776	T31120	T09344	JQ0707	A27827	S03701	T02085	S30023	JC7701	S57488	T47857	S13337	~	JC1392
	Length DB			•	•	589 2			•		380 2	•	328 2		1196 2	3144 2	168 2	347 2	858 2	300 2	436 2	1766 2		397 2			297 2	451 2	497 2	532 2
dР	Query Match Le	;	۳.		ω.		٥.	1.5	σ.	∞.	٠.	٦.	٦.	٦.		10.5				10.3			۲.	۲.			10.0	10.0	10.0	10.0
	Score	655	611		77	92	75	7	71.5	71	69	69	68.5	68.5	68.5	68.5	89	89	9	67.5	in	66.5	99	99	99	99	65.5	Ŋ.	65.5	65.5
	Result No.	п	7	m	4	2	9	7	<b>œ</b>	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	tubulin alpha chai	hypothetical prote	glucagon receptor	membrane alanyl am	hypothetical prote	cell-cycle-depende	DNA-directed RNA p	DNA-directed RNA p	coenzyme F420-depe	cellulase (EC 3.2.	qlucose 6 phosphat	hypothetical prote
AD1868	T16112	H81690	T24283	S71574	G75453	J01957	G81856	T06636	PC4035	H71529	G81686	D70669	B25156	T51467	T25413
7	~	~	7	~	~	~	~	7	N	7	~	~	~	~	7
727	1116	253	305	380	428	485	867	924	1017	1252	1252	381	409	417	444
10.0	10.0	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	9.6	9.8	9.8	g.
65.5	65.5	65	65	65	65	65	65	65	65	65	65	64.5	64.5	64.5	64.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
JORGE and Call in precursor - human cipecusor - human cipecusor - human cipecusor cannot set and care and care
```

ő

Gaps ó

ö

100.0%; Score 655; DB 2; 100.0%; Pred. No. 2.6e-61; tive 0; Mismatches 0;

Query Match
Best Local Similarity 100.0
Matches 125; Conservative

Length 185; Indels a

Page

```
parathyroid hormone-related peptide receptor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 34.4203
R;Karperien, M.; van Dijk, T.B.; Hoeijmakers, T.; Cremers, F.; Abou-Samra, A.B.; Boon submitted to the EMBL Data Library, April 1994
A;Bescription: Expression pattern of parathyroid hormone/parathyroid hormone related A;Reference number: 344203
A;Accession: 544203
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-591 <KAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tracthyroid hormone/parathyroid hormone related-peptide receptor - mouse C; Species: Mus musculus (house mouse)
C; Species: Oli-1996 #sequence_revision 02-Jul-1996 #text_change ll-Jan-2000
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change ll-Jan-2000
R; Accession: 159297
R; McCualg, K.A.; Clarke, J.C.; White, J.H.
Proc. Natl. Acad. Sci. U.S.A. 91, 5051-5055, 1994
A; Title: Molecular cloning of the gene encoding the mouse parathyroid hormone/parathy A; Reference number: 159297
A; Reference number: 159297
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: PTHR
A;Introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2;
C;Superfamily: glucagon receptor
                                               3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ů,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                         A;Cross-references: EMBL:X78936; NID:g474828; PIDN:CAA55536.1; PID:g474829
C;Superfamily: glucagon receptor
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 ARLDISSQFRKKWNKWALSRGKRELQASSSYPTGLVDEKTVPTQTL-GLQDKQSTSSTPQ 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                              1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 DVASEFRKKWNKWALSRG-KRELRM-SSSYP-----TGLADV--KAG---PAQTLIRP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 DVASEFRKKWNKWALSRG-KRELRM-SSSYP-----TGLADV--KAG---PAQTLIRP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-589 <RES>
A;Cross-references: GB:L34611; NID:9530149; PIDN:AAA40011.1; PID:9530151
C;Genetics:
Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.8%; Score 77; DB 2; Length 591; 32.5%; Pred. No. 4.3; tive 12; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 589;
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
70.0%; Score 458.5; DB 2; 72.8%; Pred, No. 1.1e-40; ive 10; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 11.6%; Score 76; DB 2
Best Local Similarity 32.5%; Pred. No. 5.4;
Matches 26; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      =
-
=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTNGHSQLPGHAKPGAPAI 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 QDMKGASRSPEDSSPDAARI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 26; Conserv
                           Similarity
                                                                                                                                                                                                                                                                                                                                       SP0GY 143
                                                                                                                                                                                                                                                                                          SPQGY 125
                                                    91;
  Query Match
Best Local S:
Matches 91
                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                    139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ω
                                                                                                                                             ద
                                                                                                                                                                                            ò
                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                          á
                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Keywords: amidated carboxyl end
E;1-21/Domain: signal sequence #status predicted <SIG>
E;2-185/Product: proadrenomedullin #status predicted <PEU>
F;22-41/Product: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F;24-41/Product: proadrenomedullin #status predicted <MAT>
F;44-Modified site: amidated carboxyl end (Arg) (amide in mature form from following gly F;143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 11-Jul-1997
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 11-Jul-1997
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 11-Jul-1997
R;Sakata, J.: Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T Biochem. Blophys. Res. Commun. 195, 921-927, 1993
A;Title: Molecular cloning and biological activities of rat adrenomedullin, a hypotensiv A;Reference number: JN0766; MUID:93384621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-185 <SAK>
A; Residues: 1-185 <SAK>
A; Accession: PN0610
A; Molecule type: protein
A; Molecule type: protein
C; Comment: This precursor contains a unique 20-amino acid sequence designated proadrenom essure control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA
                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C;Accession: S41600
E;Accession: S41600
A;Accession: S41600; MUID:94139945
A;Accession: S41600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
                                                                                                                                             Gaps
                      1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 ARLDVAAEFRKKWNKWALSRGKRELRLSSSYPTGIADLKAGPAQTVIRPQDVKGSSRSPQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-188 <KIT>
A,Cross-references: GB:D14875; NID:g439721; PIDN:BAA03590.1; PID:g496379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 611; DB 2; L
Pred. No. 1.1e-56;
8; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.3%;
91.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adrenomedullin precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 91.2 Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   adrenomedullin - pig
                                                                                                                                                                                                                                                               SPOGY 146
                                                                                                                                                                                                                SPQGY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPOGY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPOGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                 82
                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                               142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142
                                                                                                                                                                                                                                                                                                                                    RESULT 2
S41600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
                                                                  g
                                                                                                                                                              셤
                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                        õ
                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                  ò
```

÷.

```
ALZOUAL
ALZOUAL
ALZOUAL
ALZOUAL
ALZOUAL
ALZOUAL
ALZOUAL
ALZOUAL
N'Contains: fibrinopeptide B
N'Contains: fibrinopeptide B
C;Species: Petromyzon marinus
C;Species: Petromyzon
C;Date: 25-oct-1987 #sequence_revision 19-Feb-1999 #text_change 13-Aug-1999
C;Date: 25-oct-1987 #sequence
C;Date: Species
R;Dochemistry 25, 6512-6516, 1986
A;Recession: A25052
A;Molecule type: MUD: 87076582
A;Molecule type: MRNA
A;Residues: 39-479 & ACB A; A26-438, 1976
A;Title: Amino acid sequences of lamprey fibrinopeptides A and B and characterization
A;Reference number: A0310; MUD: 77065679
A;Title: Amino acid sequences of lamprey fibrinopeptides A and B and characterization
A;Reference number: A03124
A;Molecule type: protein
A;Residues: 1-36 <COT1>
A;Molecule type: protein
A;Residues: 37-42 <COT2>
A;Molecule type: protein
A;Residues: 37-42 <COT2>
A;Molecule type: protein
A;Residues: 37-42 <COT2>
A;Molecule type: protein
A;Residues: 1-36 <COT1>
A;Molecule type: protein
A;Residues: 1-36 <COT2>
C;Superfamily: fibrinogen beta chain #status experimental <CNPD>
C;Superfamily: fibrinogen beta chain #status experimental
C;Reywords: blood coagulation; glycoprotein; sulfate (Tyr) (covalent) #status experimental
F;27-A70/Product: fibrinogen beta/gamma homology <FROPS-
F;27-Binding site: sulfate (Tyr) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                 320 VRSEYRLRRADGSW-AWYIDVGQPRFSADGTFLGYVGSVLDITERRAAE-IAQQEAQAFI 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276 RVDGSSNFARDWNTYKAEFGNIAFGNGKSICNIPGEYWLGTKTVHQLTKQHTQQVLFDMS 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                           5 VASEFRKK-----WNKWALSRGKRELRMSSS---YPTGLADVKAGPAQTLIRPQDMKGAS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 RSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 RLDVASEFRKKWNKW-----ALSRGKRELRMSSSYPTGLADV----KAGPAQTLIRPQ 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 DMKG------ASRSPEDSSPDAARIRVKRYRQSMNN--FQGLRSFGCRFGTCTVQKLAH
                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27;
                                                                                                                                                                                                                       Length 1051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
          PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59;
                                                                                                                                                                                                                                                                                         63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.9%; Score 71.5; DB 2; 26.3%; Pred. No. 13;
                                                                                                                                                                                                                       5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coagulation factor V precursor [validated] - human
                                                                                                                                                                                                                Score 75; DB 2; Pred. No. 13; 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Mismatches
   A,Reference number: A96039; MUID:21368234;
A,Contents: annotation
C,Genetics:
A,Gene: SMa1548
                                                                                                                                                                                                                11.5%; 26.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 QIYQFT--DKDKDNVAP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           407
                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 36; Conserv
                                                                                                                                                  A; Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conserved hypothetical protein SWa1548 [imported] - Sinorhizobium meliloti (strain 1021) Conserved hypothetical protein SWa1548 [imported] - Sinorhizobium meliloti C;Species: Sinorhizobium meliloti C;Species: Sinorhizobium meliloti C;Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001 C;Accession: C95567 R;Seating, D.H.; Palm, C.; Perck, M.C.; Surzycki, R.; Wells, D.H.; Palm, C.; Perck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001 A;Fitle: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A95262; MUID:21396509; PMID:11481432 A;Reference number: A95262; MUID:21396509; PMID:11481432 A;Residues: 1-1051 KUR> A;Residues: 1-1051 KUR> A;Residues: 1-1051 KUR> A;Residues: 1-1051 KUR> A;Cross-references: GB.AE006469; PIDN:AAK65501.1; PID:g14523974; GSPDB:GN00165 A;Residues: 1-1051 KUR> A;Cross-references: GB.AE006469; PIDN:AAK65501.1; PID:g14523974; GSPDB:GN00165 A;Residues: 1-1051 KUR> A;Cross-references: GB.AE006469; PIDN:AAK65501.1; PID:g14523974; GSPDB:GN00165 A;Residues: 1-1051 KUR> A;Ruthors: Kahn, D; Chain, P; Comie, A; Authors: Kahn, D; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, Hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Weils, D.H.; Weidner, S.; Wells, C., Lelaure, A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
                                                                                                                                                                                                                                                                                                                                                C; Species: Rattus norvegicus (Norway rat)
C; Species: C2-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 11-Jan-2000
C; Accession: 154195; A42698
R; Pausova, Z.; Bourdon, J.; Clayton, D.; Mattei, M.G.; Seldin, M.F.; Janicic, N.; Rivier Benonics 20, 20-26, 1994
A; Title: Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor (and rat genomes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Crossrect and a composition of a common receptor for parathyroid hormone and parathyroid A;Reference and inositol trisphosphates and increases intracellular free calcium. A;Hibis Expression cloning of a common receptor for parathyroid hormone and parathyroid A;Reference number: A42698; MUID:92212903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
2
   463 NVQAEIRKSWSRWTLALDFKRKARSGSSSYSYGPMVSHTSVTNVGPRAGLSLPLSPRLLP 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 DVASEFRKKWNKWALSRG-KRELRM-SSSYP-----TGLADV--KAG---PAQTLIRP 49
                                                                                                                                                                                                                                                                                                                  parathyroid hormone/parathyroid hormone related-peptide receptor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1.585, 'G', 587-591 <ABO>
A; Experimental source: ROS 17/2.8 osteosarcoma cells
A; Note: sequence extracted from NCBI backbone (NCBIP:92187)
C; Superfamily: glucagon receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-591 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.5%; Score 75; DB 32.5%; Pred. No. 6.9; tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: 154195; MUID:94292182
A; Accession: 154195
                                                                                                                                          542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         525 ATTNGHSOLPGHAKPGA 541
                                                                                                                                       523 ATTNGHSQLPGHAKPGAPAI
                                                                 50 QDMKGASRSPEDSSPDAARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 QDMKGASRSPEDSSPDA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-585, 'G'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
쉽
                                                                 ŏ
                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

7;

ä

```
F;2065-2224/Domain: C2 <DC2>
F;2065-2224/Domain: C3 <DC2>
F;2065-2224/Domain: Gascoidin I amino-terminal homology <DN2>
F;2065-2221/Domain: discoidin I amino-terminal homology <DN2>
F;2065-2221/Domain: discoidin I amino-terminal homology <DN2, 1074,1083,1103,1106,1479, F;51,55,239,297,460,468,554,741,752,760,776,782,1231,907-2061,2066-2221/Disulfide bonds: #sta F;334-335/Cleavage site: Arg-Asn (protein C) #status predicted F;336-377/Cleavage site: Arg-Ser (coaquiation factor Xa) #status predicted F;376-377/Cleavage site: Arg-Ser (coaquiation factor Xa) #status absent F;334-355/Cleavage site: Arg-Ser (coaquiation factor Xa, thrombin) #status experiment F;1046-1047/Cleavage site: Arg-Ser (thrombin) #status experiment F;1046-1047/Cleavage site: Arg-Ser (thrombin) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTP-binding regulatory protein beta chain - wild oat
C;Species: Avena fatua (wild oat)
C;Species: Avena fatua (wild oat)
C;Accession: T08036
R;Jones, H.D.; Smith, S.J.; Desikan, R.; Plakidou-Dymock, S.; Lovegrove, A.; Hooley, Plant Cell 10, 245-254, 1998
A;Title: Heterotrimeric G proteins are implicated in gibberellin induction of a-amyla A;Reference number: 216226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-380 <10N>
A;Cross-references: EMBL:AF033357; NID:92935697; PIDN:AAC39373.1; PID:92935698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable DNA primase small subunit - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Spate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: GTP-binding regulatory protein beta chain; WD repeat homology F;245-278/Domain: WD repeat homology <WDR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 -----VRTYHGHEGDINSVKFFPDGHRFGTGSDDGTCRLFDMRIRHQLQVYSREPD 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --SSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDKDNVAPRSK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 933 LLKQSNSSKILVGRWHLAS-------EKGSYEIIQ--DTDEDTAVNNWL 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSPDAARIRVKRYRQSMNNFQGLRSF--GCRF-----GTCTV--QKLAH--QIYQFTDK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 DVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPED--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 WALSRGKRELRMSSSYPTG-LADV------KAGPAQTLIRPQDMKGASRSPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.8%; Score 71; DB 1; Length 2224; 22.6%; Pred. No. 77; tive 20; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.5%; Score 69; DB 2; Length 380; Similarity 23.6%; Pred. No. 18; Conservative 18; Mismatches 41; Indels
    F;1906-2061/Domain: discoidin I amino-terminal homology <DN1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: T08036
A; Status: preliminary: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-380 <JON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 DKDNVAP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 RNDNELP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 ISPQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         973 ISPO 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Sim:
Matches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 48-58;79-89;120-130;191-201;239-249;313-323;368-378;428-437;461-471;533-542;
2000;2111-2120;2172-2318 CGR2-
R; Jenny, R.J.; Pittman, D.D.; Toole, J.J.; Kriz, R.W.; Aldape, R.A.; Hewick, R.M.; Kaufm
Proc. Natl. Acad. Sci. U.S.A. 84, 4846-4850, 1987
A;Title: Complete cDNA and derived amino acid sequence of human factor V.
A;Reference number: A28028; MUID:87260886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-1284, 17, 1286-1600 <KAN>
A; Cross-references: GB:M1785
A; Note: parts of this sequence were determined by protein sequencing
B; Kane, W.H.; Davie, E.W.
Froc. Natl. Acad. Sci. U.S.A. 83, 6800-6804, 1986
A; Title: Cloning of a cDNA coding for human factor V, a blood coagulation factor homolog
A; Reference number: A25897; MUID:86313665
A; A; Accession: A25897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Wolecule type: mRNA
A; Residues: 1-857, 'R', 859-864, 'R', 866-924, 'E', 926-1763, 'I', 1765-2212, 'T', 2214-2224 <JEN>
A; Cross-references: GB:M16967
A; Mote: parts of this sequence, including the amino end of the mature protein, were dete
R; Kane, W.H.; Ichinose, A.; Hagen, F.S.; Davie, E.W.
Blochemistry 26, 6508-6514, 1987
A; Title: Cloning of cDNAs coding for the heavy chain region and connecting region of hum
A; Reference number: A27498; MUID:88107560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: blood coagulation
Superfamily: coagulation factor V; discoidin I amino-terminal homology; ferroxidase re
Superfamily: coagulation factor V; discoidin I amino-terminal homology; ferroxidase re
Superfamily: coagulation factor V; discoiding phospholipid binding; plasma;
12-22/A/Product: coagulation factor V #status predicted <MAT>
29-73//Product: coagulation factor V hestatus predicted <MAT>
29-73//Product: coagulation factor Va heavy chain #status experimental <VAH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 1q23-1q23
A; Introns: 53/2; 84/1; 125/1; 196/1; 244/1; 318/1; 373/2; 432/3; 466/1; 537/3; 588/1; 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description: acts as a cofactor, with calcium and phospholipid, for the factor Xa prod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Molecule type: mRNA
A.Residues: 1188-1215,1315-2224 <KA2>
A.Cross-references: GB.M14337
A.Note: parts of this sequence were determined by protein sequencing
B.Keller, F.G.; Ortel, T.L.; Quinn-Allen, M.A.; Kane, W.H.
B.Acchemistry 34, 4118-4124, 1995
A.Title: Thrombin-catalyzed activation of recombinant human factor V.
A.Reference number: A.56139; MoID:95210278
A.Contents: annotation; thrombin cleavage sites
C.Comment: Factor V is activated by thrombin and partially by coagulation factor Xa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Pathway: blood coagulation
C; Superfamily: coagulation factor V; discoidin I amino-terminal homology; ferroxide
C; Superfamily: coagulation factor V; discoidin I amino-terminal homology; ferroxide
C; Superfamily: coagulation factor V; discoidin I amino-terminal homology; ferroxide
C; Reywords: blood coagulation; predicted <SIG>
F; 12-2224/Product: coagulation factor V #status predicted <MAT>
F; 29-737/Product: coagulation factor V #status predicted <MAT>
F; 29-737/Product: coagulation factor Va heavy chain #status experimental <VAH>
F; 34-591/Domain: A1 <ADA>
F; 34-691/Domain: A2 <ADA>
F; 34-691/Domain: ferroxidase repeat homology <FO2>
F; 31-684/Domain: B <ADOB>
F; 1183-1461/Region: 9-residue repeats (Q-X-T/N-L-S-P-D-L-S)
F; 1183-1461/Region: 9-residue repeats (Q-X-T/N-L-S-P-D-L-S)
F; 1183-1461/Region: 9-residue repeats (Q-X-T/N-L-S-P-D-L-S)
                                      Species: Homo sapiens (man)
Date: 19-May-1989 #sequence_revision 02-Jun-1995 #text_change 08-Dec-2000
Accession: A55172, A42344; A28028; A27498; A25897
Cripe, L.D.; Moore, K.D.; Kane, W.H.
Accession: A55172, A585, 1992
Title: Structure of the gene for human coagulation factor V.
Reference number: A42344; MUID:92232668
N;Alternate names: coagulation labile factor; proaccelerin C;Species: Homo sapiens (man) C;Date: 19-May-1989 #sequence_revision 02-Jun-1995 #text_c}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;1574-1905/Domain: A3 <DA3>
F;181-1905/Domain: ferroxidase repeat homology <FO3>
F;1667-1765/Region: phospholipid binding #status predicted
F;1906-2064/Domain: C1 <DC1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: GDB:F5
A;Cross-references: GDB:119896; OMIM:227400
                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-2224 <CRI>
A; Cross-references: GB:J05368
A; Accession: A42344
```

7;

```
IRPQDMKGASRSPEDS----SPDAARIRV---KRYRQSMNNFQGLRSFGCRFGTCTVQK 98
  HQIYQFTDKDKDN-----VAPRSKISPQ 123
                         Query Match 10.59
Best Local Similarity 24.09
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: F56B3.4
  101
                                            237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        á
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fibrinogen beta chain precursor - rat (fragments)

N;Contains: fibrinopeptide B
C;Baces Status norvegicus (Norway rat)
C;Baces Sion: A05299; PE0010
C;Accession: A05299; PE0010
Proc. Natl. Acad. Sci. U.S.A. 81, 2313-2316, 1984
A;Title: Potential basis for regulation of the coordinately expressed fibrinogen genes: A;Reference number: A93989; MUID:84194000
A;Recession: A05299
A;Residual: 1.32 FCWA
A;Residual: 1.32 FCWA
A;Residual: A.M.; Giulla, N.B.
Gene 79, 15-158, 1989
A;Ritle: Cloining and characterization of a cDNA for the B beta chain of rat fibrinogen: A;Accession: PE0010; MUID:89378771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 33-328 < ERS>
A; Cross-references: GB:M27220; NID:g529585; PIDN:AAA41160.1; PID:g529586
C; Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfi
C; Keywords: blood coagulation; glycoprotein; liver; plasma
E; 33-65/Domain: fibrinogen disulfide ring homology (fragment) < FDR>
                Rigentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, August 1995
A;Reference number: 221815
A;Accession: T39017
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-454 <GEN>
A;Residues: 1-454 <GEN>
A;Experimental source: EMBL:298531; PIDN:CABI1078.1; GSPDB:GN00066; SPDB:SPAC6B12.10c
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           331 RLDVEVSRHINHLLKSPFCVHPGTSRVCVPIDIERMDSFNPLK-----VPTVNDLLQE 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFG------TCTVQKLA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----QDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RQDGSVDFGRKWDPYKKGFGNIATNEDTKKYCGLPGEYWLGNDKISQLTRIGPTELLIEM 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 DVASEFRKKW------NKWA----LSRGKRELRMSSSYPTGLADVKAGPAQTLIRP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RLDVASEFRKKWNKWALSRG-----KRELRMSSSYPTGLADV----KAGPAQTLIRP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31;
                                                                                                                                                                                                                                                                                                                                                                                                              36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;75-324/Domain: fibrinogen beta/gamma homology <FBG>
F;231/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63; Indels
                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                              43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.5%; Score vo...,
20.9%; Pred. No. 18;
+ive 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                            10.5%; Score 69; DB 24.4%; Pred. No. 22; tive 20; Mismatches
                                                                                                                                                                                                                                                                                                               C; Superfamily: DNA primase 50K chain
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : ||: |
L----DKNSQN 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 IYQFTDKDKDN 113
                                                                                                                                                                                                                                                  A; Gene: SPDB:SPAC6B12.10c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
C; Accession: T39017
                                                                                                                                                                                                                                                                          A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
hypothetical protein F28B23.2 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Accession: H86389
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.W.; Sun, H.; Tallo A;Title: Sequence and analysis of Chromosome I of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Status: preliminary
A;Molecule type: DNA
C. Species: Caenorhabditis elegans
C. Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C. Accession: F88632
R. Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A.Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A. Reference number: A75000; MUID: 99069613; PMID: 98191916
A.Note: see websites genome. wustl. edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A.Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A. Status: preliminary
A. Status: preliminary
A. Residues: 1-926 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Cross-references: GB:chr_IV; PIDN:AAC02615.1; PID:92854201; GSPDB:GN00022; CESP:F56 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-1196 <STO>
A;Gross-references: GB:AE005172; NID:g11079511; PIDN:AAG29222.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                555 KLEITERFDPKLLEFLKNRGNKASEETQKKPKKISKFKASRQQK -- EPENEQKGAPEPPA 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 RLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQ-DMKGASRSPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTD 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LDVASEFRKKWNK -- WALSRGKRELRMSSSYPTGLADVKAGPAQT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.5%; Score 68.5; D 22.2%; Pred. No. 54; ive 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.5%; Score 68.5; D
24.0%; Pred. No. 72;
ive 19; Mismatches
```

```
A; Molecule type: DNA
A; Residues: 1095-3144
A; Residues: 1095-3144
A; Cross-references: EMBL: 273145; MIPS:YLL040c
A; Experimental source: strain S288C
B; Lombardo, A.; Carine, K.; Scheffler, I.E.
B; Lombardo, A.; Carine, K.; Scheffler, I.E.
A; Title: Cloning and characterization of the iron-sulfur subunit gene of succinate dehych A; Reference number: A35435; MUID:90285165
A; Accession: S14891
                                                                                                                                                                                                                                                                                                  VEST3 protein - yeast (Saccharomyces cerevisiae)
VEST3 protein - yeast (Saccharomyces cerevisiae)

Nalternate names: protein L0901; protein YLL040c
C; Species: Saccharomyces cerevisiae
C; Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 13-Sep-1998
C; Accession: S64791; S14891
R; Duesterhoeft, A.; Floeth, M.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
submitted to the Protein Sequence Database, May 1996
A; Reference number: S64775
A; Accession: S64791
A; Molecule type: DNA
A; Residues: 1-1360 *PDE>
A; Residues: 1-1360 *PDE>
A; Residues: 1-1360 *PDE>
A; Residues: BMBL: 273145; MIPS: YLL040c
A; Experimental source: strain S288C
A; Experimental source: strain S288C
B; Wedder, H.; Wedler, E.; Scharfe, M.; Wambutt, R.
Submitted to the Protein Sequence Database, May 1996
A; Reference number: S64792
A; Accession: S64792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 VKRYRQ-----SMNN-----FQGLRSFGCRFG---TCTVQKLAHQIYQFTDKD----K 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.5%; Score 68.5; DB 2; Length 3144;
Best Local Similarity 28.0%; Pred. No. 2e+02;
Matches 37; Conservative 20; Mismatches 36; Indels 39; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 SRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRS----PE----DSSPDAARIR 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A) Description: involved in regulation of membrane traffic C; Keywords: transmembrane protein F;1084-1100/Domain: transmembrane *status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: SGD:VPS13; VPT2; SOI1
A;Cross-references: SGD:SO003963; MIPS:YLL040c
A;Map position: 12L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: October 17, 2002, 15:22:40 Job time : 13.8078 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 2991-3047, 'L' <LOM>
A; Cross-references: EMBL:J05487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || : |:||
1466 DNKHTELIPKSK 1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 DN----VAPRSK 119
                                                                                       99 LAHQI 103
                                                                                                                                              130 LLREL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                             g
                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                          à
```

```
October 17, 2002, 15:20:12; Search time 21.5798 Seconds (without alignments) 643.390 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Sinistry 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ARLDVASEFRKKWNKWALSR......FTDKDKDNVAPRSKISPQGY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             747574
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-018-924-2_COPY_22_146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                              Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	man adrenomeduli	man adrenomedull	Porcine adrenomedu	rcine adrenomedu	t adrenomedulin	t adrenomedullin	man secreted pro	pA(1-57)-(A)-(GS	pA(1-84)-(A)-(GS	UspA(1-56)-(DD)-(G	The squaduous demin
SUMMARIES	Desc	† 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1									AAB75123 USI	
Sul	QI S	2 AAB4	2 AAB6	2 AAB4	2 AAB6	2 AAB4	2 AAB6	1 AAGO	2 AAB7	2 AAB7	2 AAB7	22 AAB7
	Query Match Length DB ID	185 2	185 2	188 2	188 2	185 2	185 2	97 2	120 2	147 2	120 2	
dф	Query Match	100.0	100.0	93.3	93.3	70.0	70.0	58.6	45.7	44.6	44.5	43.2
	Score	655	655	611	611	458.5	458.5	384	299.5	292	291.5	283
	Result No.	-	7	m	4	S	9	7	ω	6	10	11

Composition for promoting passive elongation of vesicle smooth muscle comprises adrenomedulin  $\,$  -

WPI; 2001-080754/09. N-PSDB; AAF29138.

Yanagita T;

Claim 1; Page 26-27; 42pp; Japanese.

	Adrenomedullin pep A mutant parathyro Tethered FTH-1 rec Rat bone PTH-PTH-P Ruman lagno A human protein SEO A human protein SEO Novel human diagno Novel human diagno Novel human diagno
AAB91759 AAE09818 AAB75111 AAB75113 AAB75113 AAB75113 AAB91765 AAB91765 AAB91766 AAB91766 AAB91767	AAB01769 AAY96983 AAX96983 AAX96983 AAR92277 AAR9564 AAY9564 AAAY9866 AAM79810 AAB18668 AAM79810 AAB19073 ABG19073 ABG19073 ABG19073 ABG108359 ABG02404
788888888888888888888888888888888888888	22 22 22 22 22 22 22 23
52 52 62 170 62 63 170 63 110 83 111 311 311 311 311	2024 2024 2024 2024 2024 2024 343 343 440 440 440 440 440 440 440 44
44444444444444444444444444444444444444	41111111111111111111111111111111111111
283 283 283 283 283 283 239 231 219.5 110.5 110.5 110.4	75 75 75 75 70 70 70 68 68 68 68 68
113 114 117 118 119 119 119 120 120 120 120 120 120 120 120 120 120	7 M W W W W W W W W W W W W W W W W W W

## Passive elongation; vesicle smooth muscle; uropathic activity; adrenomedulin; urinary disorder; incontinence; human. Human adrenomedulin amino acid sequence. AAB49697 standard; Protein; 185 AA. 23-JUN-2000; 2000WO-JP04166. 99JP-0177549. (first entry) (SHIO ) SHIONOGI & CO LTD. WO200078338-A1. Homo sapiens. 23-JUN-1999; 04-APR-2001 28-DEC-2000. AAB49697; RESULT 1

ALIGNMENTS

ö

Gaps

ö

Indels

ö

Score 655; DB 22; Pred. No. 1.8e-69; ; Pred. No. 1.8 0; Mismatches

Length 185;

```
61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
                                                                                                              22 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDWKGASRSPE
                                                                                                 1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE
                                                                                                                                                                                                                                                                                                                                                                                                   Passive elongation; vesicle smooth muscle; uropathic activity; adrenomedulin; urinary disorder; incontinence; procine.
                                                                                                                                                                                                                                                                                                                                                                           Porcine adrenomedulin amino acid sequence.
represents human adrenomedullin precursor
                                                                                                                                                                                                                                                                                              AAB49698 standard; Protein; 188 AA.
                                                100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                              Best Local Similarity 100. Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprises adrenomedulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI: 2001-080754/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 AA;
                         185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAF29139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200078338-A1.
                                                                                                                                                                                                       121 SPQGY 125
                                                                                                                                                                                                                                SPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                 04-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yanagita T;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa.
                                                                                                                                                                                                                                                                                                                        AAB49698;
                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                 142
                                                                                                                                                                                                                                                                       RESULT 3
                                                                                                                                                                                                                                                                                                             ò
SXS
                                                                                                   ò
                                                                                                                          g
                                                                                                                                                                            g
                                                                                                                                                                                                                                ద
                                                                                                                                                       à
                                                                                                                                                                                                       ò
                                                                                                                                                                          . ö
          This invention relates to a composition for promoting passive elongation of vesicle smooth muscle. The composition contains adrenomedulin, and has uropathic activity. The composition can be used for promoting passive elongation of vesicle smooth muscles, this is useful for relieving urinary disorders such as impending urinary incontinence, reflex urinary incontinence, reflex urinary incontinence with overflow. The present sequence represents the human adrenomedulin protein, which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inhibiting automatic uterine contraction or contraction caused by bradykinin. The invention also relates to the use of adrenomedullin in the preparation of a drug for preventing premature birth or miscarriage. The composition of invention can be used for preventing premature birth, preventing miscarriage, stopping delivery before caesarean section or for treating dysmenorrhoea. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composition for inhibiting automatic uterine contraction or contraction caused by bradykinin comprises adrenomedullin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; adrenomedullin; precursor; bradykinin antagonist;
uterine contraction inhibitor; premature birth; miscarriage; abortion;
dysmenorrhoea; obstetric; gynaecological.
                                                                                                                                                                                                                                                                       DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
                                                                                                                                                                                Gaps
                                                                                                                                                                                                       9
                                                                                                                                                                                                                     The invention relates to a composition containing adrenomedullin for
                                                                                                                                                                                                      1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE
                                                                                                                                                                              ;
0
                                                                                                                                                   Length 185;
                                                                                                                                                                              Indels
                                                                                                                                                 100.0%; Score 655; DB 22;
100.0%; Pred. No. 1.8e-69;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 37-38; 54pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                   AAB60344 standard; Protein; 185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human adrenomedullin precursor.
                                                                                                   composition of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUN-1999; 99JP-0177548.
21-MAR-2000; 2000JP-0079171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUN-2000; 2000WO-JP04167
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SHIO ) SHIONOGI & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-080755/09.
                                                                                                                                                                  Similarity
                                                                                                                          185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAF27228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200078339-A1.
                                                                                                                                                                                                                                                                                                           SPQGY 125
                                                                                                                                                                                                                                                                                                                            SPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yanagita T;
                                                                                                                                                                Best Local Sim
Matches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                             AAB60344;
                                                                                                                             Sequence
                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                    142
                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                  82
                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                    용
ð
                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                           ð
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a composition for promoting passive elongation of vesicle smooth muscle. The composition contains adrenomedulin, and has uropathic activity. The composition can be used for promoting passive elongation of vesicle smooth muscles, this is useful for releving urinary disorders such as impending urinary incontinence, reflex urinary incontinence and urinary incontinence with overflow. The present sequence represents the porcine adrenomedulin protein, which is used in the composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                             Composition for promoting passive elongation of vesicle smooth muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 611; DB 22;
Pred. No. 3.1e-64;
8; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 31-33; 42pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 93.3%;
Local Similarity 91.2%;
nes 114; Conservative 8
23-JUN-2000; 2000WO-JP04166.
                                                                                                                                      (SHIO ) SHIONOGI & CO LTD.
```

ĺ

å g AAB6034

a

ò

```
Composition for promoting passive elongation of vesicle smooth muscle
                                                                                                                                                                                                    Passive elongation; vesicle smooth muscle; uropathic activity; adrenomedulin; urinary disorder; incontinence; rat.
                                                                                                                                                                        Rat adrenomedulin amino acid sequence
                                                                                  AAB49699 standard; Protein; 185 AA.
                                                                                                                                                                                                                                                                                                                                     23-JUN-2000; 2000WO-JP04166.
                                                                                                                                                                                                                                                                                                                                                                    99JP-0177549
                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprises adrenomedulin
                                                                                                                                                                                                                                                                                                                                                                                                (SHIO ) SHIONOGI & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-080754/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 AA;
                                                                                                                                                                                                                                               Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAF29140
                                                                                                                                                                                                                                                                            WO200078338-A1.
         142 SPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 SPQGY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPQGY 143
                                                                                                                                                                                                                                                                                                                                                                  23-JUN-1999;
                                                                                                                                            04-APR-2001
                                                                                                                                                                                                                                                                                                          28-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                              Yanagita T;
                                                                                                                AAB49699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB60346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139
                                                                    AAB49699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
                                                        RESULT
         셤
                                                                                                                pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibiting automatic uterine contraction or contraction caused by bradykinin. The invention also relates to the use of adrenomedullin in the preparation of a drug for preventing premature birth or miscarriage. The composition of the invention can be used for preventing premature birth, preventing miscarriage, stopping delivery before caesarean section or for treating dysmenorthoea. The present sequence represents porcine adrenomedullin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composition for inhibiting automatic uterine contraction or contraction caused by bradykinin comprises adrenomedullin
                                                                                                                                                                                                                                                                                                               Porcine; pig; adrenomedullin; precursor; bradykinin antagonist; uterine contraction inhibitor; premature birth; miscarriage; abortion;
                             61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
                                              81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to a composition containing adrenomedullin for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 ARLDVAAEFRKKWNKWALSRGKRELRLSSSYPTGIADLKAGFAQTVIRPQDVKGSSRSPQ 81
ARLDVAAEFRKKWNKWALSRGKRELRLSSSYPTGIADLKAGPAQTVIRPQDVKGSSRSPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 611; DB 22;
Pred. No. 3.1e-64;
8; Mismatches 3;
                                                                                                                                                                                                                                                                                                                              uterine contraction inhibitor; premature dysmenorrhoea; obstetric; gynaecological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 43-44; 54pp; Japanese.
                                                                                                                                                                                           AAB60345 standard; Protein; 188 AA.
                                                                                                                                                                                                                                                                                 Porcine adrenomedullin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.3%;
91.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUN-1999; 99JP-0177548.
21-MAR-2000; 2000JP-0079171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUN-2000; 2000WO-JP04167
                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-080755/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAF27229
                                                                                         SPQGY 125
                                                                                                                      SPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                   WO200078339-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPQGY 125
                                                                                                                                                                                                                                                     06-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                  28-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (anagita T;
                                                                                                                                                                                                                          AAB60345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
 22
                                                                                         121
                                                                                                                   142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The
```

```
;;
                                               This invention relates to a composition for promoting passive elongation of vesicle smooth muscle. The composition contains adrenomedulin, and has uropathic activity. The composition can be used for promoting passive elongation of vesicle smooth muscles, this is useful for reliaving urinary disorders such as impending urinary incontinence, reflex urinary incontinence and urinary throutinence with overflow. The present sequence represents the porcine adrenomedulin rat, which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 ARLDISSQFRKKWNKWALSRGKRELQASSSYPTGLVDEKTVPTQTL-GLQDKQSTSSTPQ
                                                                                                                                                                                                                                                                                                                                                                                                            э,
Э,
                                                                                                                                                                                                                                                                                                                                                       DB 22; Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                         70.0%; Score 458.5; DB 22; 72.8%; Pred. No. 3.7e-46; ive 10; Mismatches __21;
Disclosure; Page 37-38; 42pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB60346 standard; Protein; 185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 72.8%
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X X X X
```

g

ò

g

ô

å

```
The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.6%; Score 384; DB 21;
100.0%; Pred. No. 1.1e-37;
ive 0; Mismatches 0;
                                                                                                                                                                                                     Glordano J;
                                                                                                                                                                                                                                                                                                                                                                                      claim 13; SEQ ID 4332; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UspA(1-57)-(A)-(GSGSGDAFE)-AM-gly protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB75122 standard; Protein; 120 AA.
                                                                                                                                                                                                       Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-0CT-2000; 2000WO-JP07023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99JP-0294147
                                                                             21-FEB-2000; 2000EP-0200610
                                                                                                                     99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 DSSPDAARIRVKRYR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dumas Milne Edwards J,
                                                                                                                                                                                                                                           WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 75; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 AA;
                                                                                                                                                                                                                                                                 N-PSDB; AAC00257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200127310-A1.
                                                                                                                                                              (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                     26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-OCT-1999;
EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB75122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
AAB7512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a composition containing adrenomedullin for inhibiting automatic uterine contraction or contraction caused by bradykinin. The Invention also relates to the use of adrenomedullin in the preparation of a drug for preventing premature birth or miscarriage. The composition of the invention can be used for preventing premature birth, preventing miscarriage, stopping delivery before caesarean section or for treating dysmenorkhoea. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition for inhibiting automatic uterine contraction or contraction caused by bradykinin comprises adrenomedullin
                                                           Rat; adrenomedullin; precursor; bradykinin antagonist;
uterine contraction inhibitor; premature birth; miscarriage; abortion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSSPDAARIRVKRYRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 ARLDISSQFRKKWNKWALSRGKRELQASSSYPTGLVDEKTVPTQTL-GLQDKQSTSSTPQ 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.0%; Score 458.5; DB 22; Length 185; 72.8%; Pred. No. 3.7e-46; Live 10; Mismatches 21; Indels 3;
                                                                                                      dysmenorrhoea; obstetric; gynaecological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein, SEQ ID NO: 4332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 48-49; 54pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG00251 standard; Protein; 97 AA.
                       Rat adrenomedullin precursor.
                                                                                                                                                                                                                                                                                                           23-JUN-1999; 99JP-0177548.
21-MAR-2000; 2000JP-0079171.
                                                                                                                                                                                                                                                                     23-JUN-2000; 2000WO-JP04167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 72.8%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                         (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-080755/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 AA;
                                                                                                                                                 Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAF27230
                                                                                                                                                                                      WO200078339-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPQGY 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 SPQGY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-0CT-2000
                                                                                                                                                                                                                              28-DEC-2000,
                                                                                                                                                                                                                                                                                                                                                                                                                    Yanagita T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG00251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
```

61

ò g à g

ò

RESULT 7

ö

Gaps

ö

Length 97; Indels

```
WO200127310-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB75123;
                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4,
                                                                                                                                                                                                                                                                                                             the fused
                                                                                                                                                                                                                                                                               The present invention describes a method (M1) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 repersent sequences which are used in the exemplification of the present invention.
                                                                                                                                                             Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using recombinant host \dot{}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 ELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 DVNYSDLY-TGLIDVNLG------DMAGS------GSGDAF-----EYRQSMNNFQG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2/;
12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 LRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 299.5; DB 22;
Pred. No. 1.5e-27;
3; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UspA(1-84)-(A)-(GSGSGDAFE)-AM-gly protein.
                                                        Takimoto A, Mitsuda Y, Nakayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z
                                                                                                                                                                                                                                           Claim 17; Page 68; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB75124 standard; Protein; 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99JP-0294147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-OCT-2000; 2000WO-JP07023,
                   (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66; Conservative
                                                                                                 WPI; 2001-282044/29
N-PSDB; AAH19864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-282044/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAH19866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200127310-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB75124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE STATE OF THE S
```

```
ä
                                                          The present invention describes a method (MI) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH7510 to AAB7512 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 ELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDS-----SPDAARIRV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method (M1) for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitsushima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.6%; Score 292; DB 22; 57.0%; Pred. No. 1.5e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UspA(1-56)-(DD)-(GSGSGDAFE)-AM-gly protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17; Page 69-70; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakayama T,
Claim 17; Page 71; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB75123 standard; Protein; 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-OCT-2000; 2000WO-JP07023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-0294147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takimoto A, Mitsuda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-282044/29.
N-PSDB; AAH19865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
ses 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                    147 AA;
```

¥.

25

(first entry)

```
AAB91759 standard; Peptide;
                                                                   22-JUN-2001
                                                                                                                                                          Synthetic.
                                                AAB91759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
           RESULT 12
                    AAB91759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                      4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method (MI) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell: (b) restricted digestion of the fused protein by a protease followed by collection of sediment: and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                 Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using recombinant host \, -
                                                           Gaps
                                                                             24 ELRMSSSYPTGLADVKAGPAQTLIRPQDMKGASRSPEDSSPDAARIRVKRYRQSMNNFQG 83
                                                                                          21;
                                      DB 22; Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 52;
                                                          13; Indels
                                                                                                                   84 LRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 125
                                                                                                                               Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 283; DB 22;
Pred. No. 4.5e-26;
); Mismatches 0;
                                                Pred. No. 1.3e-26;
3; Mismatches 13
                                      Score 291.5;
exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                Takimoto A, Mitsuda Y, Nakayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75pp; Japanese.
                                                                                                                                                                                                                                               Human adrenomedullin (AM) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.2%; Scc.
100.0%; Pre
0; }
                                                                                                                                                                                      AAB75110 standard; Protein; 52 AA
                                     44.5%;
                                                                                                                                                                                                                                                                                                                                                      10-OCT-2000; 2000WO-JP07023.
                                                                                                                                                                                                                                                                                                                                                                          99JP-0294147.
                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             (SHIO ) SHIONOGI & CO LTD
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-282044/29.
N-PSDB; AAH19806.
                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                    120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 AA;
                                                                                                                                                                                                                                                                                                                 WO200127310-A1.
                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                          15-OCT-1999;
                                                         65;
                                                                                                                                                                                                                            31-JUL-2001
                                                                                                                                                                                                                                                                                                                                    19-APR-2001
                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                         AAB75110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                     Query Match
                                                  Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                    RESULT 11
AAB75110
                                                          Matches
                                                                                                                                                                                               SXS
                                                                                                                                     g
                                                                             õ
                                                                                                g
                                                                                                                   ö
```

```
The present invention describes a modified therapeutic peptide (1) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and malelmido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases in the action of peptidases to increase length of activity (half interference with physiological processes. AMB90829 to AMB92441 represent invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                         Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thibaudeau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.2%; Score 283; DB 22;
100.0%; Pred. No. 4.5e-26;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. ...
Adrenomedullin peptide (AM) SEQ ID NO:935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 498; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE09818 standard; peptide; 52 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0134406.
99US-0153406.
99US-0159783.
                                                                                                                                                                                                                                                                                                                                                                                                  17-MAY-2000; 2000WO-US13576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bridon DP, Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-112059/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 AA;
                                                                                                                                                                                                                                                                              WO200069900-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                        23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
AAE09818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ДX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

ö

Gaps

ö

Indels

Conservative

52;

Matches

ò Q



AAE09818;

```
adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rroducing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host
                                                                                                                                                                Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                       Mitsushima K;
                                                                                                                                                                                                                                                                                  The present invention describes a method (M1) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycine extended adrenomedullin (AM-gly) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitsushima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
4.6e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.2%; Score 283; DB
100.0%; Pred. No. 4.6
ive 0; Mismatches
                                                                       Nakayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 47; 75pp; Japanese.
                                                                                                                                                                                                                                            Example 1; Page 46; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB75112 standard; Protein; 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-OCT-2000; 2000WO-JP07023.
99JP-0294147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SHIO ) SHIONOGI & CO LTD.
                                     (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
nes 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takimoto A, Mitsuda Y,
                                                                         Mitsuda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-282044/29.
                                                                                                           2001-282044/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAH19808
                                                                                                                             N-PSDB; AAH19807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200127310-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-1999;
15-OCT-1999;
                                                                         Takimoto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB75112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
AAB75112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ά
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NX K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to antagonists of the vasoactive peptide calcitonin gene related peptide (CGRP) and other members of the CGRP superfamily. The invention also relates to amino the terminal modifications of peptides to improve their ability to bind to a member of the CGRP-receptor super-family. CGRP antagonists are used for inhibiting CGRP activity which can be used in vitro in assays to identify and/or isolate CGRP receptors or with intected sells either in vitro or in vivo to inhibit the effect of CGRP adrenomedullin peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vasoactive peptides useful for inhibiting calcitonin gene related
                                                                                                             Human; vasoactive peptide; calcitonin gene related peptide; CGRP; CGRP-receptor identification; adrenomedullin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YROSMNNFOGERSFECRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 YRQSMNNFQGLRSFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycine extended human adrenomedullin (AM-gly) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 283; DB 22;
Pred. No. 4.5e-26;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Column 25-26; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.2%; Sco.
100.0%; Pre
0;
                                                                       Human adrenomedullin peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB75111 standard; Protein; 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-OCT-2000; 2000WO-JP07023.
                                                                                                                                                                                                                                                                                  98US-0070504
                                                                                                                                                                                                                                                                                                                       98US-0070504
                                                                                                                                                                                                                                                                                                                                                                                                   Smith DD, Saha S, Abel PW
                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide receptor activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                             (UYCR-) UNIV CREIGHTON
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-564216/63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200127310-A1
                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                        US6268474-B1
                                                                                                                                                                                                                                                                                  30-APR-1998;
                                                                                                                                                                                                                                                                                                                       30-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JUL-2001
                                   29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-APR-2001
                                                                                                                                                                                                                                            31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52;
```

Sequence

Query Match Best Local 3 Matches AAB75111;

RESULT 14 AAB7511

g

ò

ö

Gaps

ö

ĸ

Length 53;

producing

```
ö
The present invention describes a method (M1) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment, and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                      Query Match
43.2%; Score 283; DB 22; Length 53;
Best Local Similarity 100.0%; Pred. No. 4.6e-26;
Matches 52; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                     53 AA;
                                                                                                                                                                                                                                       Sequence
    88888888888888
                                                                                                                                                                                                                                                                                                                                                                        ò
```

Search completed: October 17, 2002, 15:21:13 Job time : 22.5798 secs

g

```
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

October 17, 2002, 14:45:21; Search time 2.39401 Seconds (without alignments) 646.939 Million cell updates/sec Run on:

US-10-018-924-2\_COPY\_107\_146
219
1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		P35318 homo sapien		cani	-					-		Q9tlv1 bacteriopha							O15438 homo sapien		-	P58492 yersinia pe	xenopus 1	026346 methanobact	P30419 homo sapien	mus m	pos	P04409 bos taurus	P17252 homo sapien	mus m	P10102 oryctolagus	P05696 rattus norv	P52087 pseudomonas	060312 homo sapien
SUMMARIES	ID	ADML_HUMAN	ADML_PIG	ADML_CANFA	ADML_BOVIN	ADML_RAT	ADML_MOUSE	MRP2_RAT	MRP2_HUMAN	MRP2_RABIT	SLS6_BRAOL	VG48_BPMU	MRP4_HUMAN	G33_RAT	TYRO_RANNI	Y4KA_RHISN	SLS2_BRAOA	DNAB_RHOMR	MRP3_HUMAN	INXB_CAEEL	LI36_CAEEL	ZIPA_YERPE	PPAS_XENLA	SYH_METTH	NMT1_HUMAN	NMT1_MOUSE	NMT1_BOVIN	KPCA_BOVIN	KPCA_HUMAN	KPCA_MOUSE	KPCA_RABIT	KPCA_RAT	UVRA_PSELE	AT5C_HUMAN
	DB	H	Н	-			-4															-												-
	Query Match Length	18	188	188	188	185	184	1541	1545	1564	436	180	1325	459	532	322	435	941	1527															
æ	Query Match	100.0	97.3	92.0	92.2	89.5	85.4	27.9	26.9	25.1	24.9	23.3	23.3	23.1	23.1	22.6	22.4	22.4	22.4	22.1	22.1	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9
	Score	219	213	208	202	196	187	19	60	22	54.5	51	51	50.5	6	49.5	49	49	7	œ.	•	48											48	48
	Result No.		2	m	4	S.	91	7	œ (	ָה מי	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P56869 chlamydia m Q929a0 chlamydia p Q84317 chlamydia t Q80341 homo sapien P38808 saccharomyc Q2413 frosophila Q08415 mycobacteri P57175 buchnera ap P55049 saccharomyc P16144 homo sapien O07815 neisseria m
RPOB_CHLMU RPOB_CHLTR RPOB_CHLTR VIDE_XEAST PRII_DROME TYRO_COTA RECA_MYCFV FLIF_BUCAI FLIF_BUCAI TORI_YEAST ITB4_HUMAN RS18_NEIMA
папапапапапа
1252 1252 1252 1268 144 438 423 545 1477 1822
21.9 21.9 21.9 21.7 21.7 21.5 21.5 21.5 21.5
4 4 8 8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
48888888888888888888888888888888888888

## ALIGNMENTS

```
SEQUENCE OF 22-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45
95
153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110
                                                                                                                                                                                                                                                           KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADML_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                    PITUITARY GLAND, BOTH PEPTIDES AT PHYSIOLOGICALLY RELEVANT DOSES WINHBIT BASAL ACTI NECRETION. BOTH PEPTIDES APPEAR TO ACT IN BRAIN AND PITUITARY GLAND TO FACILITARTE THE LOSS OF PLASKA, VOLUME, ACTIONS WHICH COMPLEMENT THEIR HYPOTENSIVE EFFECTS IN BLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                          SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN PHEOCHROMOCYTOMA AND ADRENAL MEDULLA. ALSO FOUND IN LUNG, VENTRICLE AND KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADMI_PIG STANDARD; PRT; 188 AA.
P53366;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-201 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20 terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94139945; PubMed-8043068; Kitamura K., Kangawa K., Kojima M., Ichiki Y., Matsuo H., Eto T.; "Complete amino acid sequence of porcine adrenomedullin and cloning of CDNA encoding its precursor."; FEBS Lett. 338:306-310(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMIDATION (G-42 PROVIDE AMIDE GROUP). AMIDATION (G-147 PROVIDE AMIDE GROUP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADM OR AM.
Sus scrofa (Pig).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
  INHIBIT ALDOSTERONE SECRETION BY DIRECT ADRENAL ACTIONS. IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cleavage on pair of basic residues; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PREPROAM C-TERMINAL FRAGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64C7D2A0B4654DFE CRC64;
                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 219; DB 1;
100.0%; Pred. No. 2.7e-23;
:Ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADRENOMEDULLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR001710; Adrenomedullin.
Pfam: PF02039; Adrenomedullin; 1.
PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D14874; BAA03589.1; -.
EMBL; S73906; AAC60642.1; -.
EMBL; D43639; BAA07756.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20420 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Adrenal medulla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; JN0476; JN0476.
PIR; JN0684; JN0684.
PIR; JC2351; JC2351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hormone; Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41
146
185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 103275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aple, Labora e. FEBS Le' [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEPTIDE
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEPTIDE
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADML_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC OCC OC OCT REPAREMENT REPAREME
  ò
```

ĺ

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between, the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-99002704; PubMed-9788655;
Ono Y., Kojima M., Okada K., Kangawa K.;
"CDNA cloning of canine adrenomedullin and its gene expression in the heart and blood vessels in endotoxin shock.";
Shock 10:243-247(1998).
                                                                                                                                                                                                                                                                                                            -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADRENAL GLANDS, LUNG, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proadrenomedullin N-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADML_CANFA STANDARD; PRT; 188 AA.
077559; O9VTC9;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
ADM Precursor (Contains: Adrenomedullin (AM); Proadrenomedullin N-2C terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BT SIMILARITY.
AMIDATION (G-147 PROVIDE AMIDE GROUP).
AMIDATION (G-147 PROVIDE AMIDE GROUP).
71749460F5660461 CRC64;
                                                Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y., Kawamoto M., Minamino N., Matsuo H., Eto T.; Karomano M., Minamino N., Matsuo H., Eto T.; Horation and hypotensive activity of proadrenomedullin N-terminal 20 peptide (PAMP)."; FEBS Lett. 351:35-37(1994).
-1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hormone; Amidation; Cleavage on pair of basic residues; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Impto I., Jougasaki M.; "Cloning of cDNA encoding canine adrenomedullin."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                       -I- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 SFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKISPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; DB 1;
1.9e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                                                                              -1- SUBCELLULAR LOCATION: Secreted
TISSUE-Adrenal medulla;
MEDLINE-94357274; PubMed-8076689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20893 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D14875; BAA03590.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 97.5
nes 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92
146
188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41
146
188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9615;
```

```
hypotensive peptide.
                                                                                                                                                                                                                                 188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                            45
95
148
                                                                                                                                                                          110
                                                                                                                                                                                                            146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGENTS
                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                   ADML_RAT
                                                                                                                                                                          DISULFID
                                                                                                                   PEPTIDE
                                                                                                                                          PEPTIDE
                                                                                                                                                                                     MOD_RES
                                                                                                                                                                                                            MOD_RES
                                                                                                                            PROPEP
                                                                                                                                                   PROPEP
                                                                                                                                                                                                                                                                                                                                                             RESULT
    õ
                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                             PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barker S., Wood E., Clark A.J.L., Corder R.; "Cloning of bowine preproadrenomedullin and inhibition of its basal expression in vascular endothelial cells by staurosporine."; Life Sci. 62:1407-1415(1988).
FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                                                                                                     BY SIMILARITY.

AMIDATION (G-42 PROVIDE AMIDE GROUP)
(BY SIMILARITY).

AMIDATION (G-147 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                        Cleavage on pair of basic residues; Signal. 21 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                               PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                                                                                                                                                                                                                                                                                             Score 208; DB 1; Length 188; Pred. No. 9.3e-22; Indels 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                              -> K (IN REF. 2).
809D6A64F98F5578 CRC64;
                   SUBCELLULAR LOCATION: Secreted, SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CIRCULATION CONTROL (BY SIMILARITY).
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                     107 SFGCRFGTCTVQKLAHQIYQFTDNDKDGVAPRSKISPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                         1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                     ADRENOMEDULLIN
                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                          BY SIMILARIT
                                                                                                                                                                                                                                                                           SIMILARITY)
                                                                                                                                                                     InterPro; IPR001710; Adrenomedullin.
                                                                                                                                                                               Pfam; PF02039; Adrenomedullin; 1.
PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98244567; PubMed-9585168;
                                                                                                                                              EMBL; AF045773; AAD05423.1; -.
EMBL; U96127; AAD09957.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                        20929 MW;
                                                                                                                                                                                                                                                                                                                                                                              95.0%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                    38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                       92
146
188
                                                                                                                                                                                                                                                                                    115
                                                                                                                                                                                                                                                                                                                       146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
                                                                                                                                                                                                        Hormone; Amidation;
                                                                                                                                                                                                                                                                                                                                                       188 AA;
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       45
95
148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                    110
                                                                                                                                                                                                                                                                                                 41
                                                                                                                                                                                                                                                                                                                       146
                                                                                                                                                                                                                                                                                                                                              130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Aorta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADML_BOVIN
062827;
                                                                                                                                                                                                                                                                                   DISULFID
MOD_RES
                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                  PEPTIDE
PROPEP
                                                                                                                                                                                                                              PEPTIDE
                                                                                                                                                                                                                                                                                                                       MOD_RES
                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                         PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
ADML_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADM
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         å
```

```
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang X., Yue T.L., Barone F.C., White R.F., Clark R.K., Willette R.N., Sulpizio A.C., Aiyar N.V., Ruffolo R.R. Jr., Fewerstein G.Z.; "Discovery of adrenomedullin in rat ischemic cortex and evidence for its role in exacerbating focal brain ischemic damage."; Proc. Natl. Acad. Sci. U.S., 92:11480-11484(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning and biological activities of rat adrenomedullin, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20 terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                            PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY).
AMIDATION (G-147 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LUNG, KIDNEY,
                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                  Hormone; Amidation; Cleavage on pair of basic residues; Signal.
SIGNAL 1 21 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-93384621; PubMed-7690563; Sakata J., Shimokuba T., Kitamura K., Nakamura S., Kangawa K., Matsuo H., Eto T.;
                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
ADRENOMEDULLIN.
PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3002E79AB3B6612C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- TISSUE SPECIFICITY: EXPRESSED IN ADRENAL GLANDS, HEART, SPLEEN, DUODENUM AND SUBMANDIBULAR GLANDS.-i- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 202; DB 1; Leng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 SFGCRFGTCTVQKLAHQIYHFTDKDKDGSAPRSKISPOGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 195:921-927(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-SPRAGUE-DAWLEY; TISSUE=Adrenal gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY)
                                                                                                                                                           InterPro; IPR001710; Adrenomedullin. Pfam; PF02039; Adrenomedullin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
MEDLINE=96102137; PubMed=8524787;
                                                                                                                EMBL; AJ001613; CAA04866.1; -. InterPro; IPR001710; Adrenomed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20981 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.2%;
92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 92.2
Best Local Similarity 92.5
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                            41
92
146
188
                                                                                                                                                                                                                                                                                                                                                                                                                115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146
```

```
NCBI_TaxID=10116;
                                                                                                                                                                                                                        22
45
95
151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2631<u>2</u>0; 063145;
15-JUL-1998 (Rel
                                                                                                                                                                                                                                                                                                                             108
                                                                                                                                                                                                                                                                                                                                                     41
                                                                                                                                                                                                                                                                                                                                                                                         144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MRP2_RAT
                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Keppler
                                                                                                                                                                                                                             PEPTIDE
                                                                                                                                                                                                                                                                   PEPTIDE
                                                                                                                                                                                                                                                                                                                                                     MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                           MOD_RES
                                                                                                                                                                                                                                                                                         PROPEP
                                                                                                                                                                                                                                                  PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MRP2_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOD DE PHOD D
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                     Hormone, Amidation; Cleavage on pair of basic residues; Signal.

SIGNAL 1 21 BY SIMILARITY.

PROADENOMEDULIN N-20 TERMINAL PEPTIDE.

PROPEP 45 91 BY SIMILARITY.

PROPEP 94 143 ADRENOMEDULIN.

PROPEP 149 PREPROAM C.TERMINAL FRAGMENT (BY SIMILARITY).

SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              p97297; p97453;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cells at the implantation site.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                                                                                                                                                                                                                          AMIDATION (G-144 PROVIDE AMIDE GROUP) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T., Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.; Genomic organization, expression, and chromosomal mapping of the mouse adrenomedullin gene"; Genomics 37:395-399(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                      AMIDATION (G-42 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-C57BL/63;
Yotsumoto S., Ko M.S.H.;
"Expression of mouse adrenomedullin gene in trophoblastic giant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       35CAD9A9DD19AE35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SUBCELLULAR LOCATION: Secreted,
-i- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 196; DB 1,
No. 4.3e-20;
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 STGCRFGTCTMQKLAHQIYQFTDKDKDGMAPRNKISPQGY 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 AA.
                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                           Interpro; IPR001710; Adrenomedullin. Pfam; PF02039; Adrenomedullin; 1. PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-129/SV;
MEDLINE-97092892; PubMed-8938454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          20636 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.5%;
                                                                                                    EMBL; D15069; BAA03665.1; -. EMBL; U15419; AAB60519.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                     112
                                                                                                                                                                                                                                                                                                                                                                                                                 143
                                                                                                                                                                                                                                                                                                                                                                          47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                 143
                                                                                                                                                                                                                                                                                                                                                     107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADML MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADML_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        유
```

```
ö
entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. SIALN-SPRAGUE-DAWLEY, TISSUE-Liver; STRAIN-SPRAGUE-DAWLEY, TISSUE-Liver; Ito K., Suzuki H., Hirohashi T., Kume K., Shimizu T., Suglyama Y.; Expression of the putative ATP-binding cassette region, homologous to that in multidrug resistance associated protein (MRP), is hereditarily
                                                                                                                                                                                                                                                                                                   PROADEENOMEDULLIN N-20 TERMINAL PEPTIDE.
BY SIMILARITY.
PREBROAM C'TERMINAL FRAGMENT (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "cDN cloning of the hepatocyte canalicular isoform of the multidrug resistance protein, cMrp, reveals a novel conjugate export pump deficient in hyperbilirubinemic mutant rats.";
J. Biol. Chem. 271:15091-15098(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buechler M., Koenig J., Brom M., Kartenbeck J., Spring H., Horie T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Canalicular multispecific organic anion transporter 1 (Multidrug resistance-associated protein 2) (Canalicular multidrug resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARÍTY.

AMIDDATION (G-42 PROVIDE AMIDE GROUP)

(BY SIMILARITY).

(BY SIMILARITY).

(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-WISTAR; TISSUE-Liver;
MEDLINE-96180672; PubMed=8599091;
Paulusma C.C., Bosma P.J., Zaman G.J.R., Bakker C.T.M., Otter M.,
Scheffer G.L., Scheper R.J., Borst P., Oude Elferink R.P.J.;
"Congenital jaundice in rafs with a mutation in a multidrug
resistance-associated protein gene.";
Science 271:1126-1128(1996).
                                                                                                                                                                                             Pfam; PF02039; Adrenomedullin; 1.
PRINTS; PR00801; ADRENOMEDULN.
Hormone; Amidation; Cleavage on pair of basic residues; Signal.
SIGNAL 1 21 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> G (IN REF. 2).
C88C99045A79C898 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 187; DB 1;
Pred. No. 7.5e-19;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1541 AA
                                                                                                                                            MGD; MGI:108058; Adm.
InterPro; IPR001710; Adrenomedullin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-WISTAR; TISSUE-Liver;
MEDLINE-96279006; Pubmed-8662992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABCC2 OR CMOAT OR MRP2 OR CMRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20764 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 85.4%;
Local Similarity 85.0%;
les 34; Conservative
                                                                                       EMBL; D78349; BAA11367.1;
                                                                                                                    AAB36535.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                     41
92
144
184
                                                                                                                                                                                                                                                                                                                                                                                                                                                        113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
```

D5FB55571BFDDB39 CRC64;

173383 MW;

1541 AA;

```
SEQUENCE
                                                                                                                                                                                                    RESULT 8
MRP2_HUMAN
           တ္ထ
                                                                                                                 οy
                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                  SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE LIVER.
DISEASE: DEFECTS IN ABCC2 ARE A CAUSE OF HEREDITARY CONJUGATED HYPERBILLIRUBINEMIA (EHBR).
SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
                  Int. Hepatol. Commun. 292:292-299(1996).
-!- FUNCTION: MEDIATES HEPATOBILIARY EXCRETION OF NUMEROUS ORGANIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (BY SIMILARITY).
2 (YYOPLASHIC (BY SIMILARITY).
2 (EW SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
CYTOPLASHIC (BY SIMILARITY).
CYTOPLASHIC (BY SIMILARITY).
4 (BY SIMILARITY).
5 (BY SIMILARITY).
CYTOPLASHIC (BY SIMILARITY).
CYTOPLASHIC (BY SIMILARITY).
CYTOPLASHIC (BY SIMILARITY).
CYTOPLASHIC (BY SIMILARITY).
7 (BY SIMILARITY).
7 (BY SIMILARITY).
CYTOPLASHIC (BY SIMILARITY).
CYTOPLASHIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat.
DOMAIN 1 26 EXTRACELLUIAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
9 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 (BY SIMILARITY).

EXTRACELLULAR (BY SIMILARITY).

11 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
13 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (BY SIMILARITY).
15 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (BY SIMILARITY).
17 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC...) (I
N-LINKED (GLCNAC...) (I
N-LINKED (GLCNAC...) (I
N-LINKED (GLCNAC...) (I
M -> V (IN REF. 3).
defective in Eisai hyperbilirubinemic rats (EHBR).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                              EMBL; L49379; AAC42087.1; -
EMBL; X96393; CAA65257.1; -
EMBL; D86086; BAA13016.1; -
HSSP; P13569; 1NBD.
InterPro; IPR0013593; AAA.
InterPro; IPR00140; ABC_transporter_tmem.
InterPro; IPR00140; ABC_transporter_tmem.
InterPro; IPR001403; APC_GTP_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam: PF00664; ABC_membrane; 2.
Pfam: PF00005; ABC_tran; 2.
SMART: SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11114
11115
11207
1228
1230
1230
1251
1541
674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              561
583
604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48
68
89
                                                     ANIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
NP_BIND
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
 RATE TO THE TEST OF THE TEST O
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tsujii H., Koenig J., Rost D., Stoeckel B., Leuschner U., Keppler D., "Exon-intron organization of the human multidrug-resistance protein 2 (MRP2) gene mutated in Dubin-Johnson syndrome."; Gastroenterology 117:653-660(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEDINBE-98087571; PubMed=9425227; WEDINBE-98087571; PubMed=9425227; WEDINBE-98087571; PubMed=9425227; Wakamura T., Uchiumi T., Kohno K., Yoshida M., Toh S., Taniguchi K., Adachi Y., Kuwano M.; Mutations in the canillicular multispecific organic anion transporter (CMOAT) gene, a novel ABC transporter, in patients with hyperbilirubinemia II/Dubin-Johnson syndrome."; Hum. Mol. Genet. 7:203-207(1998).
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96390592; PubMed=8797578;
MEDLINE=96390592; PubMed=8797578;
Taniguchi K., Wada M., Kohno K., Nakamura T., Kawabe T., Kawakami M., Ragotani K., Okumura K., Akiyama S., Kuwano M.;
"A human canalicular multispecific organic anion transporter (CMOAT) gene is overexpressed in cisplatin-resistant human cancer cell lines with decreased drug accumilation.";
Cancer Res. 56:4124-4129(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Kool M., de Haas M., Ponne N.J., Paulusma C.C., Oude-Elferink R.P.J.,
Baas F., Borst P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "cbNa cloning of the hepatocyte canalicular isoform of the multidrug
resistance protein, cMrp, reveals a novel conjugate export pump
deficient in hyperbillirubinemic mutant rats.";
J. Biol. Chem. 271:15091-15098(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buechler M., Koenig J., Brom M., Kartenbeck J., Spring H., Horie T.,
                                                                                                                                                                                                                                                                                                                                                          MRP2_HUMAN STANDARD;
9PT; 1545 AA.
902887, 092798; 014022; 092500; 09UMS2;
15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
16-COT-2000 (Rel. 40, Last annotation update)
Canalicular multispecific organic anion transporter 1 (Multidrug resistance-associated protein 2) (Canalicular multidrug resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS DJS TRP-768 AND ARG-1382.
MEDLINE-99162196; PubMed-10053008;
Toh S., Wada M., Uchiumi T., Inokuchi A., Makino Y., Horie Y.,
      DB 1; Length 1541;
                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keppler D.; Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases
                                                                 17;
                                                                                                                                                                        Pred. No. 2.2;
4; Mismatches
                                                                                                                                  6 FGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABCC2 OR CMOATI OR CMOAT OR MRP2 OR CMRP.
      Score 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99395001; PubMed-10464142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=96279006; Pubmed=8662992;
   27.9%;
38.2%;
Query Match 27.9
Best Local Similarity 38.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Keppler D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS
```

1)

```
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
realistance-associated protein 2) (Canalicular multidrug resistance protein) (Epithelial basolateral chloride conductance regulator).
ABCC2 OR MRP2 OR EBCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                               10 (BY SIMILARITY).

EXTRACELLULAR (BY SIMILARITY).

I1 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).

12 (BY SIMILARITY).

13 (BY SIMILARITY).

13 (BY SIMILARITY).

14 (BY SIMILARITY).

14 (BY SIMILARITY).
                                                 2 (BY SIMILARITY).
EXTRACELULAR (BY SIMILARITY).
3 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
4 (BY SIMILARITY).
5 (BY SIMILARITY).
5 (BY SIMILARITY).
5 (BY SIMILARITY).
                                                                                                                                                                                       6 (BY SIMILARITY).

EXTRACELLULAR (BY SIMILARITY).

7 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).

8 (BY SIMILARITY).

9 (BY SIMILARITY).

9 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LO (HX SIMILARITY).

ENTRACELULAR (BY SIMILARITY).

17 (BY SIMILARITY).

CYTOPLASHIC (BY SIMILARITY).

ATP (POTENTIAL).

ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 59, DB 1; Length 1545;
Pred. No. 4.2;
5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLUIAR (BY SIMILARITY).
15 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
16 (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY)
                  1 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1483 FAHCTVITIAHRLHTIMDSDKVWVLDNGKIIECGSPE 1519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGTCTVQKLAHQIYQFTDKDKDNVAPRSKI----SPQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.9%;
ilarity 37.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
11118
11140
11211
1232
1234
1255
1545
1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1188
1430
1515
1545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Simi
Matches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MRP2_RABIT
Q28689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
NP_BIND
NP_BIND
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
DOMAIN
                                                                                                                                                                                                               DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
                                                     TRANSMEM
DOMAIN
                                                                                                        DOMAIN
TRANSMEM
                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                    RANSMEM
                                                                                                                                                                                                                                                                                                                                                                     FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                           FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                    FRANSMEM
                                                                                                                                                                                              TRANSMEM
                                                                                         FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MRP2_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-sib.ch).
 PROSITE; PS00211; ABC_TRANSPORTER; 1.
ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003593; AAA.
InterPro; IPR001140; ABC_transporter_tmem.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AJ132244, CAB45309.11
- AJ132287, CAB45309.11
- AJ132288, CAB45309.11
- AJ132289, CAB45309.11
- AJ132289, CAB45309.11
- AJ132289, CAB45309.11
- AJ132291, CAB45309.11
- AJ132292, CAB45309.11
- AJ132293, CAB45309.11
- AJ132294, CAB45309.11
- AJ132295, CAB45309.11
- AJ132295, CAB45309.11
- AJ132295, CAB45309.11
- AJ132295, CAB45309.11
- AJ132296, CAB45309.11
- AJ132296, CAB45309.11
- AJ132299, CAB45309.11
- AJ132309, CAB45309.11
- AJ132309, CAB45309.11
- AJ132301, CAB45309.11
- AJ1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00664; ABC_membrane; 2.
Pfam; PF00005; ABC_tran; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AJ132300; CAB45309; I) JUN 132300; CAB45309; I) JUN 132301; CAB45309; I) JUN 132302; CAB45309; I) JUN 132304; CAB45309; I) JUN 132306; CAB45309; I) JUN 132306; CAB45309; I) JUN 132306; CAB45309; I) JUN 132309; CAB45309; I) JUN 132310; CAB45309; I) JUN 132311; CAB45309; I) JUN 132311; CAB45309; I) JUN 132311; CAB45309; I) JUN 132313; CAB45309; II) JUN 132313; CAB45309; I
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U63970; AAB39892.1; -. EMBL; U49248; AAB09422.1; -. EMBL; X96395; CAA65259.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; P13569; 1NBD.
601107; -.
237500; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disease mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
```

ä

Gaps

4

Ŋ

```
CARBOHYD
           DOMAIN _
TRANSMEM
                                DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oleracea.
   TRANSMEM
                                                    DOMAIN
NP_BIND
NP_BIND
                                                                                 CARBOHYD
                                                                                             CARBOHYD
                                                                                                                                     Query Match
                                                                                                                                                        Matches
                                                                                                                                                                                                                                         SLS6_BRAOL
                                                                                                                                                                            9
                                                                                                                                                                                                                              RESULT 10
   844444444
                                                                                                                                                                            δ
                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
                                       van Kuijck M.A., van Aubel R.A.M.H., Busch A.E., Lang F., Russel F.G.M., Bindels R.J.M., van Os C.H., Deen P.M.T.; "Molecular Coloning and expression of a cyclic AMP-activated chloride conductance regulator: a novel ATP-binding cassette transporter."; Proc. Natl. Acad. Sci. U.S.A. 93:5401-5406(1996).
                                                                                                                                              by
in
                                                                                                                                                                                                     -i- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
                                                                                                                                                                        MOI. Pharmacol. 53:1062-1067(1998).
-!- FUNCTION: MEDIATES HEPATOBILIARY EXCRETION OF NUMEROUS ORGANIC
                                                                                                                       van Aubel R.A.M.H., van Kuijck M.A., Koenderink J.B., Deen P.M.T.,
van Os C.H., Russel F.G.M.;
                                                                                                                                          "Adenosine triphosphate-dependent transport of anionic conjugates the rabbit multidrug resistance-associated protein Mrp2 expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLUIAR (BY SIMILARITY).

1 (BY SIMILARITY).

2 (BY SIMILARITY).

2 (BY SIMILARITY).

EXTRACELLUIAR (BY SIMILARITY).

3 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).

4 (BY SIMILARITY).

EXTRACELLUIAR (BY SIMILARITY).

6 (BY SIMILARITY).

EXTRACELLUIAR (BY SIMILARITY).

6 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 (BY SIMILARITY).

EXTRACELLULAR (BY SIMILARITY).

7 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).

8 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (BY SIMILARITY).
9 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
14 (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (BY SIMILARITY).
12 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (BY SIMILARITY).
10 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR003553; AAA.
Interpro; IPR001140; ABC_transporter_tmem.
Interpro; IPR00349; ABC_transportr.
Interpro; IPR001687; ATE_GTP_A.
Pfam; PF00064; ABC_membrane; 2.
Pfam; PF00005; ABC_tran; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00211; ABC_TRANSPORTER; 1
                                                                                                             MEDLINE-98279125; PubMed-9614209;
                             MEDLINE-96224297; PubMed-8643587;
                                                                                                                                                                                                                                                                                                                                       EMBL; 249144; CAA89004.1; -. HSSP; P13569; 1NBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        542
563
585
606
969
990
1031
1052
1095
1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00382; AAA;
[1]
SEQUENCE FROM N.A.
                                                                                                                                                               cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1032
1053
1096
1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                    TISSUE-Ileum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RANSMEM
                                                                                                                                                                Insect
                                                                                                                                                                                                                                                                                                                                                                                                                                                      OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERRATUM.

Nasrallah J.B., Kao T.-H., Goldberg M.L., Nasrallah M.E.;

Nature 326:523-523(1987).

'I- FUNCTION: INVOLVED IN SPOROPHYTIC SELF-INCOMPATIBILITY SYSTEM

(THE INABILITY OF FLOWERING PLANTS TO ACHIEVE SELF-FERTILIZATION).

-!- TSSUE SPECIFICITY: STICMA.

-!- TSSUE SPECIFICITY: THERE ARE A TOTAL OF 50 DIFFERENT S ALLELES IN

B.OLERACEA.

-!- SIMILARITY: TO THE EXTRACELLULAR PORTION OF A MAIZE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nasrallah J.B., Kao T.-H., Chen C.H., Goldberg M.L., Nasrallah M.E.; "Amino-acid sequence of glycoproteins encoded by three alleles of the S locus of Brassica oleracea."; Nature 326:617-019(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nasrallah J.B., Kao T.-H., Goldberg M.L., Nasrallah M.E.;
"A cDNA clone encoding an S-locus-specific glycoprotein from Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
15 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).

16 (BY SIMILARITY).

EXTRACELLULAR (BY SIMILARITY).

17 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).

ATP (POTENTIAL).

ATP (POTENTIAL).

ATP (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

"""" NFFN (GLCNAC. ..) (POTENTIAL).
""" NFFN (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 1564;
                                                                                                                                                                                                                                                                                  NKED (GLCNAC. . .) (POTED BEBFSAC8FE45873 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
S-locus-specific glycoprotein S6 precursor (SLSG-6).
                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1481 FSHCTVITIAHRLHTIMDSDKIMVLDNGNIVEYG 1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    436 AA.
                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 15;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                          Score 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Y00268; CAA68375.1; -.
EMBL; X03170; CAA26934.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brassica oleracea (Cauliflower).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A27827; A27827.
InterPro; IPR001480; B_lectin.
InterPro; IPR003609; Pan_app.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1988 (Rel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                       25.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KINASE RECEPTOR (ZMPK1).
                                                                                                                                                                                                                                                                                                     175542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 22-435 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 318:263-267(1985).
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
          11138
1209
1230
1232
1253
1543
1543
1339
                                                                                                                                                                                                                                                                          1009
                                                                                                                                                                                                                                                                          1009 100
1564 AA;
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3712;
                                1139
1210
1231
1233
1254
669
1332
                                                                                                                                                                                                                                                                                                                                                          I Mac
Local Sind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLS6_BRAOL
```

```
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NP_BIND
       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a allcense agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                    ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Morgan G., Hatfull G., Hendrix R.;

Morgan G., Hatfull G., Hendrix R.;

"Genome of bacteriophage Mu and comparison with the Haemophilus

"Influenzae Mu-11ke prophage Fluwn.";

Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

-1- SIMILARITY: SOME, TO H.INFLUENZAE HI1521 AND SOME, TO E.COLI YMFQ.
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                    .) (POTENTIAL)..) (POTENTIAL)..) (POTENTIAL)..) (POTENTIAL)..)
                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
NCBI_TaxID=10677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                              Length 436;
                                                                                                                                S-LOCUS-SPECIFIC GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                         227 GVRFSGIPEDQKLSYMVYNFTENSEEVAYTFRMTNNSIYSRLTLSSEGY 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.3%; Score 51; DB 1; Length 180; 50.0%; Pred. No. 5.8;
                                                                                                                                                                                                                                                                                                                                                                                    3 GCRF-GTCTVQKLAHQIYQFTDKDKD------NVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                  14; Indels
                                                                                            Glycoprotein; Polymorphism; Signal.
                                                                                                                                                                                                                                                               49779 MW; E2332635B885A515 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF083977; AAF01126.1; -. SEQUENCE 180 AA; 20468 MW; 3045A6C185B48BF9 CRC64;
                                                                                                                                           N-LINED (GLCNAC...) (FN-LINED (GLCNAC...)) (FN-LINED (GLCNAC...) (FN-LINED (GLCNAC...)) (FN-LINED (GLCNAC...) (FN-LINED (GLCNAC...)) (FN-LINED (GLCNAC...) (FN-LINED (GLCNAC...)) (FN-LINED 
                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                               24.9%; Scor.
28.6%; Pred. No. 4..,
... 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1325 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
InterPro; IPR000858; Slocus_glycop.
               Pfam; PF01453, Agglutinin; 1.
Pfam; PF00954; Slocus_glycop; 1.
SWART; SW00108; Blectin; 1.
SWART; SW00473; PAN_AP; 1.
Self-incompatibility; Glycoprotea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MRP4_HUMAN STANDARD; P 015439; 09Y602; 15-7UL-1998 (Rel. 36, Created) 16-OCT-2001 (Rel. 40, Last sequile-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 CTVQKL--AHQIYQFTDKDKDN 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                  14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                            436 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriophage Mu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein gp48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VG48_BPMU
                                                                                                                                                                                   CARBOHYD
CARBOHYD
                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09T1V1;
                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
MRP4_HUMAN
                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
       ð
                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4444B
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DETOXIFICATION.
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH PARTICULARLY HIGH
LEVELS IN PROSTATE, BUT IS BARELY DETECTABLE IN LIVER.
--- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MRP SUBFAMILY.
                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Brain;
MEDLINE-97413640; PubMed-9270026;
Kool M., de Haas M., Scheffer G.L., Scheper R.J., van Eijk M.J.,
Julin J.A., Bass E., Borst P.;
"Analysis of expression of cWOAT (MRP2), MRP3, MRP4, and MRP5,
homologues of the multidrug resistance-associated protein gene
(MRP1), in human cancer cell lines.";
Cancer Res. 57:3537-3547(1997).
--- FUNCTION: MAY BE AN ORGANIC ANION PUMP RELEVANT TO CELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL). (POTENTIAL). (POTENTIAL).
Multidrug resistance-associated protein 4 (MRP/cMOAT-related ABC transporter) (MOAT-B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                              MEDLINE-98324262; PubMed-9661885;

Lee K., Belinsky M.G., Bell D.W., Testa J.R., Kruh G.D.;

"Isolation of MoAr-B, a widely expressed multidrug resistance-

associated protein/canalicular multispecific organic anion

transporter-related transporter.";

Cancer Res. 58:2741-2747(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Transmembrane; Transport; Repeat. 93 113 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (
N-LINKED (
N-LINKED (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003593; AAA.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; APP_GTP_A.
Pfam; PF00005; ABC_tran; 2.
Pfam; PF00064; ABC_membrane; 2.
SWART; SM00382; AAA; 2.
PROSITE; PS00211; ABC_TRANSPORTER; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1155-1316 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF071202; AAC27076.1; -.
EMBL; U8366); AAB11757.1; -.
HSSP; P13569; 1NBD.
MIM; 605250; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      460
730
730
730
856
878
878
974
1058
1058
1082
651
651
651
746
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                      NCBI_TaxID=9606;
                           transporter) (
ABCC4 OR MRP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSOC
ATP-binding;
```

```
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /ARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ETAL
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the BMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                       ö
                                                                                                                                                                                  01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 36, Last annotation update)
Rene 33 polypeptide.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                          Chrapkiewicz N.B., Davis C.M., Chu D.T.W., Granner D.K.; "Rat gene 33: analysis of its structure, messenger RNA and basal promoter activity.";
. .) (POTENTIAL)
. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5,
                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 459;
                                                                                                                                                                                                                                                                                                                                                                      STRAIN=SPRAGUE DANLEY; TISSUE-Liver;
MEDLINE-89138017; PubMed=3224831;
AIIdal M-H., Lee K.L., Isham K.R., Cadilla C., Kenney F.T.;
"Structure of a multihormonally regulated rat gene.";
Gene 71:413-420(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                         1- INDUCTION: BY CAMP, GLUCOCORTICOIDS, PHORBOL ESTERS AND
                                                   Length 1325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                       Indels
                    > D (IN REF. 2).
9C5750A748BB96CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        459 AA; 49941 MW; EBD90F11757AC549 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
 N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ¥.
                                                                                                                                                               459 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RISSCT----HRASPSSDEDKPEIPPRVPIPPR 290
                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQ 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 50.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            532
                                                  Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 17:6651-6667(1989)
                      ۵
^
                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M23570; AAB08828.1; JOINED. EMBL; M23571; AAB08828.1; JOINED.
                                                                                                                                                                                                                                                                                                  MEDLINE=89385990; PubMed=2780291;
                               MM;
                                                                                                              1222 KFAHCTVLTIAHRLNTIIDSDK 1243
                                                                                      5 RFGTCTVQKLAHQIYQFTDKDK 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYRO_RANNI STANDARD; E 004604; 01-OCT-1993 (Rel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X07266; CAA30252.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.1%;
32.4%;
                              1325 AA; 149539
                                                   23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB08828.1; -
                                                            40.98;
                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Conservative
                                                                                                                                                                STANDARD;
 1176
1309
1302
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S03116; S03116.
                                                             Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                           NCBI_TaxID-10116;
1176
1309
1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M23572;
                                                                                                                                                                                                                                                                                                                                                                                                                                    INSULIN
 CARBOHYD
          CARBOHYD
                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                      CONFLICT
                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local
                                                                                                                                                               G33_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
TYRO_RANNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                           RESULT 13
 EEES
                                                                                           ŏ
                                                                                                              셤
                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Miura I., Okumoto H., Makino K., Nakata A., Nishloka M.; Analysis of the tyrosinase gene of the Japanese pond frog, Rana nigromaculata: cloning and nucleotide sequence of the genomic DNA containing the tyrosinase gene and its flanking regions.", Jpn. J. Genet. 70:79-82(1995).
-I. FUNCTION: THIS IS A COPER-CONTAINING OXIDASE THAT FUNCTIONS IN THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
                                                                                                                                             Euteleostomi;
Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COPPER A (BY SIMILARITY).
COPPER A (BY SIMILARITY).
COPPER B (BY SIMILARITY).
N-LINKED (GLONAC...) (POTENTIAL).
N-LINKED (GLONAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOPAGUINONE + H(2)O.
-! -COFACTOR: BINDS TWO COPPER IONS.
-! -SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.
-! -SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase).
                                                                                                                                                                                                                                                                            MEDILINE-93077054; PubMed-1446833; Takase M., Miura I., Nakata A., Takeuchi T., Nishioka M.; Takase M., Miura I., Nakata A., Takeuchi T., Nishioka M.; Toloning and sequencing of the cDNA encoding tyrosinase of the Japanese pond frog, Rana nigromaculata."; Gene 121:359-363(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LUMENAL, MELANOSOME (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B27D3080F0C74B3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GLCNAC. . .) (GLCNAC. . .) (GLCNAC. . .)
                                                                                                            Rana nigromaculata (Japanese pond frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 50.5; 1
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYROSINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Melanin biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; JC1392; JC1392.
InterPro; IPR00227; Tyrosinase.
Pfam; PF00264; tyrosinase; 1.
PRINTS; PR00092; TYROSINASE.
PROSITE; PS00497; TYROSINASE.
PROSITE; PS00499; TYROSINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Blood;
MEDLINE-95290234; PubMed-7772385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60115 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D12514; BAA02077.1; -. EMBL; D37779; BAA07034.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE OF 1-277 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                532 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                      NCBI_TaxID=8409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
20
20
476
500
184
206
2215
3371
394
115
                                                                                       TYR OR TYRS
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                        Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A., Perret X.;
                                                                                                                                                                                                                                                                          Plasmid sym pNGR234a.
Bacteria: Proteobacteria: alpha subdivision: Rhizobiaceae group;
     13;
                                                                                                                                                                                                                                                                                                                                                                                                                      Molecular basis of symbiosis between Rhizobium and legumes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 322;
   9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Indels
                                                  4 CRFG----TCTVQK--LAHQIYQFTDKDKD-----NVAPRSKISP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .EMBL; AE000081; AAB91733.1; -. Hypothetical protein; Plasmid. SEQUENCE 322 AA; 36690 MW; 177BOAF61FA0C74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                             Y4KA_RHISN STANDARD; PRT; 322 AA. P55521; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) Hypothetical 36.7 kDa protein Y4KA.
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.6%; Score 49.5; D
35.3%; Pred. No. 17;
tive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-97305956; PubMed-9163424;
   8;
                                                                                                                                                                                                                                                            Rhizobium sp. (strain NGR234).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 387:394-401(1997).
-!- SIMILARITY: NONE OBVIOUS.
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Conservative
                                                                                                                                                                                                                                                                                                           Rhizobiaceae; Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=394;
16;
                                                                                                                               Y4KA_RHISN
 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                              RESULT 15
                                                               셤
                                 õ
```

210 GQPKVNKLADEI-QFTTKNSFSATPSAELDPANH 242

oy da Search completed: October 17, 2002, 14:49:12 Job time : 4.39401 secs

7 GTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40

1 3

```
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

October 17, 2002, 14:45:20 ; Search time 4.58853 Seconds (without alignments) 837.648 Million cell updates/sec

US-10-018-924-2\_COPY\_107\_146
219
1 SFGCRFGTCTVQKLAHQIXQFTDKDKDNVAPRSKISPQGY 40 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

Total number of hits satisfying chosen parameters: 283138 seqs, 96089334 residues

283138

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	יייי ביין ביין ביין ביין ביין ביין ביין	į,,	adrenomedullin pre	•		multidrng resistan	9	ı	S-locus-specific a	S-locus-specific a	7	٠.	S-10002 Specific g	-Specific	-locus-specific	_	S-100m-specific	S-locus-specific a	-receptor kinase	-locus-specific	-locus-spec	hypothetical prote				ARC Transhorter AR	thetical nr	probable g-recent	hynothetical prote	4
SUMMARIES	QI	JN0684	S41600	JN0766	T14536	S71839	S71841	A99638	A85489	T14415	T14529	G84107	T07814	A27827	T14424	T14423	T15540	T14416	T14530	T07809	T07810	T14528	E91004	E85637	. 520799	T14533	AD2000	T16368	T14471	0	
	DB	N	7	~	7	Н	Н	7	7	7	~	~	~	7	7	7	~	7	7	7	N	~	7	~	7	7	~	7	7	~	
	Query Match Length	185	188	185	430	1541	1545	189	189	431	428	373	428	436	427	428	465	428	428	429	426	429	93	93	319	429	809	759	857	171	
σŧ	Query				28.1		26.9	26.7					24.9		24.4							23.5									
	Score	219	213	196	61.5	61	59	58.5	58.5	58.5	55.5	22	54.5	54.5	53.5	53.5	53	52.5	52.5	52.5	51.5	51.5	21	21	51	51	51	51	51	50.5	
	Result No.	1	7	က	4	2	9	7	ω.	σ,	10	11	12	13	14	15	16	. 17	18	19	20	21	22	23	24	25	56	27	28	58	

hypothetical prote gene 33 protein, h	monophenol monooxy hypothetical prote	S-receptor kinase	hypothetical prote	myb-related transc hypothetical prote	exonuclease SbcC   hypothetical prote	hypothetical prote	conserved hypothet	sugar phosphate nu	S-locus-specific g
T27938 S03116	JC1392 S58319	T14472	C86279	T51674 T05996	AB0551 T47067	T48354 C97389	AD2607	F90507	T0/812
7.79	7	~ -	2	7 7	77	0 0	~	0	N
419 459	532 587	850	00.5	250	1034	356	204	253	4 3 T
23.1 23.1	23.1 23.1	23.1	22.8	22.8	22.8	22.6	22.4	22.4	4.77
50.5	50.5	50.5	20	200	50 49.5	49.5	64.	4. 4 20 C	4,
30	33 33	34	36	38	39 40	41	43	4.4	4

## ALIGNMENTS

RESULT 1

JN0684
dictioned in precursor   Industrial Crispecies: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
:
Systems Biophys. Res. Commun. 203, 631-639, 1994
A; Title: Genomic structure of human adrenomedullin gene.
A; Reference number: JC2351; MUID:94354869
A.Molecule type: DNA
A; Residues: 1-185 <ish></ish>
A; Cross-references: GB:S73906; NID:9765329; PIDN:AAC60642.1; PID:9765330
A; Experimental source: pheochromocytoma
Rikitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.
Autochem Biophys Res. Commun. 194, 720-725, 1993. Affilled Cloning and characterization of only consists.
A; Reference number: JN0684; MILD: 93343928
A; Accession: JN0684
A; Molecule type: mRNA
A) Kesidues: 1-185 <kit></kit>
A:Cross-reletences: GB:D148/4; NID:9455470; PIDN:BAA03589.1; PID:9500612
A. A. C. C. C. S. S. C.
A.Molecute 17pc: Plotein A.Residues: 22-41 <kt2></kt2>
R;Kitamura, K.; Kanqawa, K.; Kawamoto, M.; Ichiki, Y.: Nakamura, S.: Matsuo, H.: Pro
Biochem. Biophys. Res. Commun. 192, 553-560, 1993
A; Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocy
A; Reference number: JN0476; MUID:93249425
A;Accession: JN0476
A; Molecule type: protein
A; Residues: 95-146 < KI3>
A; Experimental source: pheochromocytoma
C;Genetics:
A, delle: GDB, SALDM A. Chass-reference: CDB, 211010. Outw. 102246
A: WED DOS! #100 - 1 10+0-1-1 10+0-1
A; Introds: 33/2; 83/2
C; Keywords: amidated carboxyl end: blood pressure control: hormone
F;1-21/Domain: signal sequence #status predicted <sig></sig>
F;22-185/Product: proadrenomedullin #status predicted <peu></peu>
F:32-41/Domain: proadrenomedullin amino-terminal 20 peptide #status predicted <pap></pap>
1.75. 1407-100 autonomicantin status experimental AMAIN- F:147-185/Domain: Carboxyl-forminal properties estatus aveainted
F:41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following
F;110-115/Disulfide bonds: #status experimental
F;146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following

ó

Gaps

; 0

Query Match 100.0%; Score 219; DB 2; Length 185; Best Local Similarity 100.0%; Pred. No. 8.8e-23; Matches 40; Conservative 0; Mismatches 0; Indels

ರ

```
canalicular multicarug resistance procesin - ract
C.Species: Rattus norvegicus (Norway rac)
C.Species: Rattus norvegicus (Norway rac)
C.Species: Rattus norvegicus (Norway rac)
C.Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C.Accession: S71839
J. Spucoller, M.; Koenig, J.; Brom, M.; Kartenbeck, J.; Spring, H.; Horle, T.; Keppler,
J.; Biol. (Chem. 271, 15091-15098, 1996
A; Title: cDNA cloning of the hepatocyte canalicular isoform of the multidrug resistan
A; Reference number: S71839; MUD:96279006
A; Reference number: S71839; MUD:96279006
A; Residues: Preliminary; nucleic acid sequence not shown
A; Molecule type: manAA
A; Residues: 1-1541 - GBUE>
A; Cross-references: EMBL:X96393; NID:91292881; PIDN:CAA65257.1; PID:91617207
C; Scuperfamily: human multidrug resistance protein cWOA72; ATP-binding cassette homolo
C; Keywords: ATP; 91ycoprotein; nucleotide binding; P-loop; transmembrane #status predicted <TW01>
F; 100-124/Domain: transmembrane #status predicted <TW02>
F; 100-124/Domain: transmembrane #status predicted <TW05>
F; 305-329/Domain: transmembrane #status predicted <TW05>
F; 314-451/Domain: transmembrane #status predicted <TW05>
F; 356-364/Domain: transmembrane #status predicted <TW05>
F; 366-944/Domain: transmembrane #status predicted <TW05>
F; 366-944/Domain: transmembrane #status predicted <TW05>
F; 366-944/Domain: transmembrane #status predicted <TW05>
F; 314-451/Domain: transmembrane #status predicted <TW05>
F; 3104-1132/Domain: transmembrane #status predicted <TW05>
F; 1014-1132/Domain: transmembrane #status predicted <TW07>
F; 1104-1132/Domain: transmembrane #status predicted <TW07>
F; 1104-1132/Domain: transmembrane #status predicted <TW07>
F; 1104-1132/Domain: transmembrane #status predicted <TW08>
F; 1104-1132/Domain: transmembrane 
                                                                                                                                                                                                                                                                                                   A;Residues: 1-430 <KUS>
A;Cross-references: EMBL:D85212; NID:g2351155; PIDN:BAA21946.1; PID:g2351156
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Reywords: glycoprotein
                                                                        o
F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;6,1007,1010,1011/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             multidrug resistance protein, canalicular - human
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
C;Accession: S71841; S71840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 1541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 GIRFSGIPEDEKLSYMVYNFTENNEEVAYTFRMTNNSIYSRLTVSPEGY 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GCRF-GTCTVQKLAHQIYQFTDKDKD------NVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 61.5; DB 2;
Pred. No. 1.4;
                                                                                                                                                                                             A, Accession: T14536
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     canalicular - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1479 FSQCTVITIAHRLHTIMDSDKIMVLDNGKIVEYG 1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        canalicular multidrug resistance protein - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 FGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 27.9%; Score 61;
Best Local Similarity 38.2%; Pred. No. 4
Matches 13; Conservative 4; Mismatch
                                                                                                                                                       A; Reference number: Z18078; MUID: 97352858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 28.6%;
Matches 14; Conservative 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
                                                                                                                         echanism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 22-41 <SA2>
C;Comment: This precursor contains a unique 20-amino acid sequence designated proadrenom
essure control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F.1-21/Domain: signal sequence #status predicted <SIG>
F.22-185/Product: proadrenomedullin #status predicted <PEU>
F.22-185/Product: proadrenomedullin amino-terminal 20 peptide #status predicted <PE>
F.34-147/Product: adrenomedullin amino-terminal 20 peptide #status predicted <PE>
F.34-147/Product: adrenomedullin #status predicted <PE>
F.34-147/Product: adrenomedullin #status predicted <PE>
F.34-147/Prodicted site: amidated carboxyl end (Tyr) (amide in mature form from following gly F:143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adrenomedullin precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 11-Jul-1997
C;Accession: JN0766; PN0610
R;Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T R;Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T R;Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T R;Sakata, J.; Shimokubo, T.; Kitamura, M.; Sillian and Diological activities of rat adrenomedullin, a hypotensiv A;Accession: JN0766; MUID:93384621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA encd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: $ glycoprotein
C;Species: Brassica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C;Accession: T14536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Complete amino acid sequence of porcine adrenomedullin and cloning A;Reference number: $41600; MUID:94139945 A;Accession: $41600
                                                                                                                                                                                                                                                                                                       direnomedullin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C;Accession: S41600
C;Accession: K; Kangawa, K.; Kojima, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
FEBS Lett. 338, 306-310, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: mRNA
Residues: 1-180 <KIT>
A;Cross-references: GB:D14875; NID:g439721; PIDN:BAA03590.1; PID:g496379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-locus-specific glycoprotein - wild cabbage (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 STGCRFGTCTMQKLAHQIYQFTDKDKDKDGMAPRNKISPQGY 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 SFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKISPQGY 146
                                                                                          SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 196; DB 2;
Pred. No. 1.4e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 213; DB 2;
Pred. No. 6.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :Keywords: amidated carboxyl end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 89.5%;
l Similarity 87.5%;
35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 97.3%;
1 Similarity 97.5%;
39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-185 <SAK>
A; Accession: PN0610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 39; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                             107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
                                                                                                                                                                                                                                              RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            α
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                         g
                                                            à
```

```
A.Accession: A85489
A.Status: preliminary
A.Molecule type: DNA
A.Rolecule type: DNA
A.Rosidus: 1-189 CSTO>
A.Cross-references: GB:AE05174; NID:g12512769; PIDN:AAG54373.1; GSPDB:GN00145; UWGP:
A.Experimental source: strain 0157:H7, substrain EDL933
C.Genetics:
A.Gene: Z0078
C.Superfamily: Escherichia coli yabp protein
                                    iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5-10cus-specific glycoprotein - wild cabbage (fragment)
N;Alternate names: S glycoprotein
N;Alternate names: S glycoprotein
C;Decies: Brassica oleracea (wild cabbage)
C;Dete: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C;Accession: T14529
R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons of cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
C;Molecule type: DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Rosidues: 1-428 cxtus>
A;Cross-references: EMBL:D85205; NID:g2351141; PIDN:BAA21939.1; PID:g2351142
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Accession: T14415
R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C'Species: Brassica rápá (turnip)
C'Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 26.7%; Score 58.5; DB 2; Length 431; Best Local Similarity 32.7%; Pred. No. 3.7; Matches 16; Conservative 8; Mismatches 14; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 GVRFSGMPGDQKLNYMYYNFTENSEDVAYTFRMTNKSIYSRLKISSEGF 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GCRF-GTCTVQKLAHQIYQFTDKDKD------NVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S-locus-specific glycoprotein - turnip (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - || | : :| : || :|:| || 95 KLTHWLIKFNELKEYAKDPENMAAKASLSPEG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 58.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 KLAHQIYQFTD----KDKDNVAPRSKISPQG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                echanism.
A:Reference number: 218078; MUID:97352858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: Z18078; MUID:97352858
A; Accession: T14529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 26.7%;
Best Local Similarity 34.4%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N; Alternate names: S glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: T14415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 echanism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                         A; Accession: $7184;
A; Roclecule type: mRNA
A; Residues: 1.1545 < KODS
A; Residues: 1.1545 < KODS
A; Cross references: EMBL: X96395; NID:g1507819; PIDN:CAA65259.1; PID:g1514568
A; Cross references: EMBL: X96395; NID:g1507819; PIDN:CAA65259.1; PID:g1514568
B; Buechler, M.; Koenig, J.; Brom, M.; Kartenbeck, J.; Spring, H.; Horie, T.; Keppler, D.
Biol. Chem. 271, 15091-15098, 1996
A; Title: CDNA cloning of the hepatocyte canalicular isoform of the multidrug resistance
A; Reference number: 871839; MUID:96279006
A; Accession: S71840
A; Status: nucleic acid sequence not shown
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1415-1429, 'VP', 1432-1455, 'E', 1457-1545 < BUE>
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A'Gene: GDB.ABCC2; CMOAT; ABC; MRP2; CMRP; DJS
A'Cross-references: GDB:6089489; OMIM:601107
A'Map position: 10924-10924
C'Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology C'Keywords: ATP; glycoprotein; nucleotide binding; P-loop; transmembrane protein
F:654-87/Pomain: ATP-binding cassette homology cABC1>
F:671-678/Region: nucleotide-binding motif A (P-loop)
F:1317-1510/Domain: ATP-binding cassette homology cABC2>
F:1334-1341/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein ECs0073 [imported] - Escherichia coli (strain O157:H7, substrain RI Cispecies: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: Bs-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 (Spacession: A99638 R: Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Basawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc A; Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein 20078 [imported] - Escherichia coli (strain O157:H7, substrain EDLG C; Species: Escherichia coli (c) Paceis: Escherichia coli (c) Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C; Accession: A885489 R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-189 <-HAY>
A; Cross-references: GB:BA000007; PIDN:BAB33496.1; PID:g13359529; GSPDB:GN00154
A; Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 26.9%; Score 59; DB 1; Length 1545; Best Local Similarity 37.8%; Pred. No. 12; Matches 14; Conservative 5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 1483 FAHCTVITIAHRLHTIMDSDKVMVLDNGKIIECGSPE 1519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 FGTCTVQKLAHQIYQFTDKDKDNVAPRSKI----SPQ 38
R;Koenig, J.; Keppler, D.
submitted to the EMBL Data Library, August 1996
A;Reference number: S71841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 58.5; D
Pred. No. 1.6;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 KLAHQIYQFTD----KDKDNVAPRSKISPQG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Genetics:
A;Gene: Ecs0073
C;Superfamily: Escherichia coli yabP protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 26.7%;
Best Local Similarity 34.4%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
```

 $_{\rm cl}$ 

Length 428;

DB 2;

Score 55.5;

```
S-locus-specific glycoprotein - turnip (fragment)
N.Alternate names: S glycoprotein
C.Species: Brassica rapa (turnip)
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C.Accession: T14423
R.Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons of classical processions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Modecule type: DNA
A; Residues: 1-428 <KUS>
A; Cross-references: EMBL:D85223; NID:g2351177; PIDN:BAA21957.1; PID:g2351178
A; Cross-references: EMBL:D85223; Siperial of the construction of the constructio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             o f cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:D85225; NID:92351181; PIDN:BAA21959.1; PID:92351182
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein
                 S locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S-locus-specific glycoprotein - turnip (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica rapa (turnip)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C;Accession: T14424
R;Kusaba, M; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
R;Kusaba, M; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3
                    the
          A;Title: Amino-acid sequence of glycoproteins encoded by three alleles of the A;Title: Amino-acid sequence of glycoproteins encoded by three alleles of the A;Reference number: A3392
A;Recession: A27827
A;Rolecule type: MAS>
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein C;Keywords: glycoprotein
F;1-31,Domain: slgnal sequence #status predicted <SIG>F;3-436/Product: S-locus-specific glycoprotein S6 #status predicted <MAT>F;40-434/Domain: S-locus-specific glycoprotein homology <SSG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 427;
                                                                                                                                                                                                                                                                                                                                                                                       Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GCRF-GTCTVQKLAHQIYQFTDKDKD------NVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GCRF-GTCTVQKLAHQIYQFTDKDKD------NVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
24.4%; Score 53.5; DB 2;
Best Local Similarity 28.6%; Pred. No. 18;
Matches 14; Conservative 10; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: T14423
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: T14424
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-427 < KUS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.4%; Score 53.5; D
28.6%; Pred. No. 18;
tive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      pred. No. 13;
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          24.9%; Score 54.5; 28.6%; Pred. No. 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: 218078; MUID: 97352858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: 218078; MUID:97352858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 28.6%
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 28.69
Matches 14; Conservative
326, 617-619, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
T14424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-locus-specific glycoprotein S6 - radish (fragment)
C;Species: Raphanus sativus (radish)
C;Species: Raphanus sativus (radish)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Accession: T07014
R;Sakamoto, K:; Kusaba, M:; Nishio, T.
Mol. Gen. Genet. 258, 397-403, 1998
A;Title: Polymorphism of the S-locus glycoprotein gene (SLG) and the S-locus related gen
A;Reference number: 216146; MUID:98311079
                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
R;Accession: 684107
R;Takami, H: Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: DNA
A;Residues: 1-373 <STO>
A;Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07382.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
                                                                                                                                                                                                                                                                                                                                      c-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology C;Reywords: glycoprotein C;Reywords: glycoprotein F;32-426/Domain: S-locus-specific glycoprotein homology <SSG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                          lipopolysaccharide biosynthesis BH3663 [imported] - Bacillus halodurans (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-428 <SAK>
A; Cross-references: EMBL:AB009682; NID:g3327849; PIDN:BAA31729.1; PID:g3327850
                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A27827
S-locus-specific glycoprotein S6 precursor - wild cabbage
C;Species: Barssica oleracea (wild cabbage)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 15-Nov-1996
C;Accession: A27827
R;Nasrallah, J.B.; Kao, T.H.; Chen, C.H.; Goldberg, M.L.; Nasrallah, M.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 GIRFSGIPEDQKLSYMVYNFTENSEEVAYTFLMTNNSIXSRLTISSSGY 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GCRF-GTCTVQKLAHQIYQFTDKDKD------NVAPRSKISPQGY 40
                                                                                                                                                        219 GVRFSGIPENQKLSYMVINFTENSEEVAYTFRMINNSFYSRLKVSSDGY 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 373;
                                                                                                               ----NVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 54.5; I
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55; DB Pred. No. 9.7
                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 GFGAVYKLAHQIVSLSEGVKENLVRRYKI 156
                        .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCTVQKLAHQIYQFTDKDKDNVAPRSKI 35
                        Pred.
                                                                                                                  GCRF-GTCTVQKLAHQIYQFTDKDKD---
                                                    8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.9%;
milarity 30.6%;
Conservative 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.18;
                 30.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 13; Conserv
                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: T07814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Genetics:
A;Gene: SLG(S6)
                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: BH3663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                           Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                              Matches
                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                           g
```

qq ŏ

Search completed: October 17, 2002, 14:46:17 Job time: 7.58853 secs

THIS PAGE BLANK (USPTO)

٠

>

Adrenomedullin pep Rat adrenomedulin Rat adrenomedulin Rat adrenomedulin Adrenomedullin pep Adrenomedullin pep Adrenomedullin pep Adrenomedullin pep Human preproadreno Adrenomedullin pep

AAB60346 AAB91767 AAB91761 AAB91765 AAW25160 AAB91762 AAE09827 AAE09827

Porcine adrenomedu

AAB60345 AAE09819 Rat canalicular mu Human CMOAT C-term Multi-drug resista Human canalicular

AAB11449 AAB28224

AAW33362 AAW55966

Human preproadreno Drosophila melanog Drosophila melanog Drosophila melanog Drosophila melanog

ABB65954 ABB59224

Clas I S-locus gly Clas I S-locus gly Clas I S-receptor Drosophila melanog Drosophila melanog Novel human diagno

AAW56307 ABB62270 ABB60761 ABG05415

ABB65953 AAW56306

ABB63391

ABG09129 AAW58582 ABG14932 ABG10411 ABB66152

ABG13273

Kojibiose phosphor Novel human diagno Novel human diagno

Orosophila melanog

ALIGNMENTS

Novel human diagno Novel human diagno

```
AAB75110 standard; Protein; 52 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                              1541
231
231
1545
1545
                                                                                                                                                                                                         13
1302
1344
1327
1346
                                                                                                                                                                                                                                                              436
846
892
1348
229
229
677
775
939
939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-282044/29.
N-PSDB; AAH19806.
WO200127310-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JUL-2001
 AAB75110;
                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB75110
 Glycine extended h
Glycine extended a
Linker peptide-adr
UspA(1-57) (A) (GS
UspA(1-56) (DD) (G
UspA(1-49) (A) (GS
Thioredoxin (GSGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adrenomedullin pep
Human adrenomedull
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human adrenomeduli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human adrenomedull
                                                                     October 17, 2002, 14:45:20; Search time 9.67581 Seconds (without alignments) 459.181 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                      A_Geneseq_032802:*

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseqy-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseqy-embl/AA1982.DAT:*
| SIDSI/gcgdata/geneseqy-embl/AA1982.DAT:*
| SIDSI/gcgdata/geneseqy-embl/AA1984.DAT:*
| SIDSI/gcgdata/geneseqy-embl/AA1986.DAT:*
| SIDSI/gcgdata/geneseqy-embl/AA1986.DAT:*
| SIDSI/gcgdata/geneseqy-embl/AA1986.DAT:*
| SIDSI/gcgdata/geneseqy-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqy-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1990.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1996.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1996.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1996.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1999.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                          747574
                                                                                                                                             40
                                                                                                                              219
1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
        GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                   fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                747574 segs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                     US-10-018-924-2_COPY_107_146
                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                 - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB75113
AAB75122
AAB75123
AAB75124
AAB75114
AAB75114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB75111
AAB75112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB75110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE09818
                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52
52
52
53
53
53
62
120
1170
1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0
100.0
100.0
100.0
100.0
100.0
                                                                                                                            Perfect score:
                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219
219
219
219
219
219
219
219
219
                                                 OM protein
                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                Searched:
                                                                                                                                          Sequence:
                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
```

```
Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host
                                                                  Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           χ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitsushima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takimoto A, Mitsuda Y, Nakayama T,
Human adrenomedullin (AM) protein.
                                                                                                                                                                                                                                                                                                                                                        10-OCT-2000; 2000WO-JP07023.
                                                                                                                                                                                                                                                                                                                                                                                                                       99JP-0294147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SHIO ) SHIONOGI & CO LTD
```

```
AAE09818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                              ò
8888888888
                                                                                                                                                                         à
                                                                                                                                                                                                 셤
                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (III) (e.g. succinimidy) and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptides stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                         producing the fused
                       The present invention describes a method (MI) for producing darenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 repersent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thibaudeau K;
                                                                                                                                                                                         Length 52;
                                                                                                                                                                                                                   Indels
                                                                                                                                                                                       Score 219; DB 22;
Pred. No. 2.5e-24;
                                                                                                                                                                                                                                                          1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holmes DL,
                                                                                                                                                                                      Query Match
100.0%; Score 219; I
Best Local Similarity 100.0%; Pred. No. 2.5
Matches 40; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      Adrenomedullin peptide (AM) SEQ ID NO:935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 498; 733pp; English.
    Page 45; 75pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Milner PG,
                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                         AAB91759 standard; Peptide; 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0134406.
99US-0153406.
99US-0159783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAY-2000; 2000WO-US13576
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-112059/12.
                                                                                                                                                                 52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200069900-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                              22-JUN-2001
        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bridon DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                     AAB91759;
                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                  RESULT 2
                                                                                                                                                                                                                                                                                                                             AAB91759
                                                                                                                                                                                                                                                                                                                                                                                                           q
        8×00000000000x8
                                                                                                                                                                                                                                                  à
```

```
ö
Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           calcitonin gene related peptide (CGRP) and other members of the CGRP superfamily. The invention also relates to amino the terminal modifications of peptides to improve their ability to bind to a member of the CGRP-receptor super-family. CGRP antiquists are used for inhibiting CGRP activity which can be used in vitro e.g. in assays to identify and/or isolate CGRP receptors or with intact cells either in vitro or in vivo to inhibit the effect of CGRP binding to its receptor. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vasoactive peptides useful for inhibiting calcitonin gene related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; vascactive peptide; calcitonin gene related peptide; CGRP; CGRP-receptor identification; adrenomedullin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to antagonists of the vasoactive peptide
                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 40; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                             ; Score 219; DB 22;
; Pred. No. 2.5e-24;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                             1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                   Claim 5; Column 25-26; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human adrenomedullin peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE09818 standard; peptide; 52
                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saha S, Abel PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0070504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0070504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide receptor activity
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adrenomedullin peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYCR-) UNIV CREIGHTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-564216/63
                                                                                                                                                                                                                                                              Best_Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 AA;
                                                                                                                                                                                       52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6268474-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JUL-2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE09818;
                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13
```

ö

1

AAB75111;

AAB75111 RESULT

```
Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a
                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a method (M1) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications, AAH19806 to AAH19866 and AAB75110 to AAB75124 repersent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Linker peptide-adrenomedullin (AM) precursor protein.
                                                                                                                                                                                                     Mitsuda Y, Nakayama T, Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 219; DB 22;
100.0%; Pred. No. 2.6e-24;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 47; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Æ
                                                                                                                                                                                                                                                                                                                 application comprises producing recombinant host -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB75113 standard; Protein; 62
                                                                                                                           99JP-0294147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-OCT-2000; 2000WO-JP07023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-0294147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SHIO ) SHIONOGI & CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                       WPI; 2001-282044/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-282044/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 AA;
                                                                                                                                                                                                                                                              N-PSDB; AAH19808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAH19809
             WO200127310-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200127310-A1.
                                                                                      10-OCT-2000;
                                                                                                                             15-0CT-1999;
                                                                                                                                                                                                    Takimoto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-1999;
                                                    19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB75113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a method (MI) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications, AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host -
                                                                                                                                                                                        Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                   Glycine extended human adrenomedullin (AM-gly) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pakimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycine extended adrenomedullin (AM-gly) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 219; DB 22;
100.0%; Pred. No. 2.6e-24;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 46; 75pp; Japanese.
                                         AAB75111 standard; Protein; 53 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
                                                                                                                                                                                                                                                                                                                                                            10-OCT-2000; 2000WO-JP07023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB75112 standard; Protein;
                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-282044/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAH19807
                                                                                                                                                                                                                                                                                  WO200127310-A1
                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
Synthetic.
                                                                                                                 31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JUL-2001
                                                                                                                                                                                                                                                                                                                       19-APR-2001
```

40;

Matches

13

a

ò

RESULT 5

AAB75112;

Sequence

Query Match

ö

Gaps

ö

52

Length 53; Indels

ø

```
The present invention describes a method (M1) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19806 and AAB75110 to AAB75124 represent sequences which are used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a
                                                                                                               The present invention describes a method (M1) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications, AAH19806 to AAH19866 and AAB75110 to AAB75124 repersent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
 rrouncing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using recombinant host
                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitsushima K;
                                                                                                                                                                                                                                                                                                                          Score 219; DB 22;
Pred. No. 3.1e-24;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                              SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                SPGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UspA(1-57)-(A)-(GSGSGDAFE)-AM-gly protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 17; Page 68; 75pp; Japanese.
                                                                                    75pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB75122 standard; Protein; 120
                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2000; 2000WO-JP07023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-0294147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takimoto A, Mitsuda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-282044/29
                                                                                    Page 48;
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                           62 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAH19864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200127310-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                    Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB75122;
                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB75122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                  ð
```

```
ö
                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method (MI) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment: and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                       Adrenomedullin; glycine extended adrenomedullin; AM: AM-gly;
adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                           ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 120;
                                                   Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 219; DB 22;
100.0%; Pred. No. 6.6e-24;
iive 0; Mismatches 0;
                                                                                                                     80 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitsushima
                                                   22;
                                                                                                      1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                              ö
                                                               6.6e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                   DB
                                                                                                                                                                                                                                                                              UspA(1-56)-(DD)-(GSGSGDAFE)-AM-91y protein.
                                                                              Mismatches
                                                 Score 219;
Pred. No. 6
exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takimoto A, Mitsuda Y, Nakayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Page 69-70; 75pp; Japanese.
                                                                                                                                                                                                  Ą
                                                   100.0%; Sc
100.0%; P1
tive 0;
                                                                                                                                                                                                 AAB75123 standard; Protein; 120
                                                                                                                                                                                                                                                                                                                                                                                                                                        10-OCT-2000; 2000WO-JP07023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99JP-0294147
                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-282044/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 AA;
                          120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-282044
N-PSDB; AAH19865
                                                                                                                                                                                                                                                                                                                                                                                      WO200127310-A1
                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-OCT-1999;
                                                                                                                                                                                                                                                     31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40;
                                                                                                                                                                                                                                                                                                                                                                                                               19-APR-2001
                                                                                40;
                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                             Seguence
                                                                                                                                                                                                                           AAB75123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                Matches
                                                                                                                                                                           æ
                                                                                                                                                                         RESULT
                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                 ద
  SXS
                                                                                                           ò
```

ó;

Gaps

0; 62;

RESULT 9

AAB75124

Synthetic

```
adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 repersent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                              Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition for promoting passive elongation of vesicle smooth muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Passive elongation; vesicle smooth muscle; uropathic activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adrenomedulin; urinary disorder; incontinence; human
                                                                                                                                                                                       Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method (M1) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 219; DB 22;
1larity 100.0%; Pred. No. 9.8e-24;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human adrenomedulin amino acid sequence.
                                                                                                                                                                                       Nakayama T,
                                                                                                                                                                                                                                                                                                                                                      Claim 17; Page 49-50; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB49697 standard; Protein; 185
                                                                   10-OCT-2000; 2000WO-JP07023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUN-2000; 2000WO-JP04166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-0177549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                     Mitsuda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprises adrenomedulin
                                                                                                                                              OD 9 IDONOIHS ( OIHS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-080754/09.
N-PSDB; AAF29138.
                                                                                                                                                                                                                         WPI; 2001-282044/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 AA;
                                                                                                                                                                                                                                           N-PSDB; AAH19810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200078338-A1
                                                                                                      15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                  rakimoto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUN-1999;
                               19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yanagita T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB49697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method (MI) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host
                                                                                                                                                    Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; glycine extended adrenomedullin; AM; AM-gly;
precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ķ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitsushima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 219; DB 22; Similarity 100.0%; Pred. No. 8.3e-24; 0; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                            UspA(1-84)-(A)-(GSGSGDAFE)-AM-gly protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thioredoxin-(GSGSGDAFE)-AM-gly protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takimoto A, Mitsuda Y, Nakayama T,
AAB75124 standard; Protein; 147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; Page 71; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB75114 standard; Protein; 170
                                                                                                                                                                                                                                                                                                                                            10-OCT-2000; 2000WO-JP07023
                                                                                                                                                                                                                                                                                                                                                                                   99JP-0294147
                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-282044/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAH19866
                                                                                                                                                                                                                                                                   WO200127310-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adrenomedullin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200127310-A1.
                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                 15-OCT-1999;
                                                                           31-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens.
                                                                                                                                                                                                                                                                                                        19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JUL-2001
```

AAB75114;

RESULT 10

g à

Synthetic

Sequence Query Match

Local Best Loca Matches

ö

Gaps

ö

Indels

Length 170;

the fused

producing

ö

Gaps

ö

Indels

ö

Mismatches

. 0

Conservative

40;

```
Matches
                                                         g
                                á
                                                                                                                                                                                                                                            ö
                                      This invention relates to a composition for promoting passive elongation of vesicle smooth muscle. The composition contains adrenomedulin, and has uropathic activity. The composition can be used for promoting passive elongation of vesicle smooth muscles, this is useful for relieving urinary disorders such as impending urinary incontinence, reflex urinary incontinence and urinary incontinence with overflow. The present sequence represents the human adrenomedulin protein, which is used in the composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibiting automatic uterine contraction or contraction caused by bradykinin. The invention also relates to the use of adrenomedulin in the preparation of a drug foor preventing premature birth or miscarriage. The composition of the invention can be used for preventing premature birth, preventing miscarriage, stopping delivery before caesarean section or for treating dysmenorthoea. The present sequence represents human adrenomedullin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition for inhibiting automatic uterine contraction or contraction caused by bradykinin comprises adrenomedullin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; adrenomedullin; precursor; bradykinin antagonist;
uterine contraction inhibitor; premature birth; miscarriage; abortion;
dysmenorrhoea; obstetric; gynaecological.
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a composition containing adrenomedullin for
                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                Length 185;
                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                 ; DB 22;
1.1e-23;
                                                                                                                                                                                                                                                                                            1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                 100.0%; Score 219;
                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54pp; Japanese
                 Claim 1; Page 26-27; 42pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                     AAB60344 standard; Protein; 185
                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human adrenomedullin precursor.
                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JUN-1999; 99JP-0177548.
21-MAR-2000; 2000JP-0079171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUN-2000; 2000WO-JP04167
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 37-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-080755/09
                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 AA;
                                                                                                                                                                                    185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAF27228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200078339-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yanagita T;
                                                                                                                                                                                                                                                40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     AAB60344;
                                                                                                                                                                                      Seguence
                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                           107
                                                                                                                                                                                                                                                                                                                                                                        AAB60344
                                                                                                                                                                                                                                                                                                                                                                                                                      g
      ò
```

Length 185;

Score 219; DB 22; Pred. No. 1.1e-23;

100.0%;

Local Similarity

Query Match Best Local

THE E

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to a composition for promoting passive elongation of vesicle smooth muscle. The composition contains adrenomedulin, and has uropathic activity. The composition can be used for promoting passive elongation of vesicle smooth muscles, this is useful for releving urinary disorders such as impending urinary incontinence, reflex urinary incontinence and urinary incontinence with overflow. The present sequence represents the porcine adrenomedulin protein, which is used in the composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition for promoting passive elongation of vesicle smooth muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Porcine; pig; adrenomedullin; precursor; bradykinin antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Passive elongation; vesicle smooth muscle; uropathic activity; adrenomedulin; urinary disorder; incontinence; procine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 SFGCRFGTCTVQKLAHQIYQFTDKDKDKDGVAPRSKISPQGY 146
                                         107 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 213; DB 22;
Pred. No. 8.2e-23;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                             Porcine adrenomedulin amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 31-33; 42pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB60345 standard; Protein; 188 AA
                                                                                                                                                                                                                                         ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Porcine adrenomedullin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                         AAB49698 standard; Protein; 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.3%;
97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUN-2000; 2000WO-JP04166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprises adrenomedulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-080754/09.
N-PSDB; AAF29139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200078338-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-APR-2001
                                                                                                                                                                                                                                                                                                                                                                              04-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yanagita T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB60345;
                                                                                                                                                                                                                                                                                                               AAB49698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                              RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB60345
                                                                                                                                                                                                          AAB49698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XXEXEX XXX
                                                                                                                                                                                                                                                                                                                                                                                                                 NAME OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
```

```
Bridon DP,
                                                                                                                                                                                                                                                                                                                                          Sequence
       g
                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                      The invention relates to a composition containing adrenomedullin for inhibiting automatic uterine contraction or contraction caused by bradykinin. The invention also relates to the use of adrenomedullin in the preparation of a drug for preventing premature birth or miscarriage. The composition of the invention can be used for preventing premature birth, preventing miscarriage, stopping delivery before caesarean section or for treating dysmeorthoea. The present sequence represents porcine adrenomedullin precursor.
                                                                                                                                                                                                                                 Composition for inhibiting automatic uterine contraction or contraction caused by bradykinin comprises adrenomedullin
uterine contraction inhibitor; premature birth; miscarriage; abortion; dysmenorrhoea; obstetric; gynaecological.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 SFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKISPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 213; DB 22;
Pred. No. 8.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adrenomedullin peptide (AM) SEQ ID NO:944.
                                                                                                                                                                                                                                                                   Disclosure; Page 43-44; 54pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB91768 standard; Peptide; 40 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0134406.
99US-0153406.
99US-0159783.
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 97.3%;
Best Local Similarity 97.5%;
Matches 39; Conservative
                                                                                                                       23-JUN-1999; 99JP-0177548.
21-MAR-2000; 2000JP-0079171.
                                                                                                  23-JUN-2000; 2000WO-JP04167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000WO-US13576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUN-2001 (first entry)
                                                                                                                                                        (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                  WPI; 2001-080755/09
                                                                                                                                                                                                                                                                                                                                                                                           188 AA;
                                                                                                                                                                                                             N-PSDB; AAF27229
                                                     WO200078339-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200069900-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
Synthetic.
                                                                             28-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-NOV-2000
                                                                                                                                                                             Yanagita T;
                                 Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB91768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB91768
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
```

```
The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active anno acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active anno acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases. AMB90829 to AAB92441 represent preptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                     Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                             Thibaudeau K;
                                                                                        Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 502; 733pp; English.
                                                                                        Milner PG,
                                                                                        Ezrin AM,
(CONJ-) CONJUCHEM INC.
                                                                                                                                                                            WPI; 2001-112059/12
```

40 AA;

ö Length 40; Indels 5 DB 22; 89.5%; Score 196; DB 22 llarity 87.5%; Pred. No. 4e-21; Conservative 3; Mismatches .Query Match Best Local Similarity Matches 35; Conserv

ö

Gaps

1 SFGCRFGTCTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40

Search completed: October 17, 2002, 14:47:59 Job time: 11.6758 secs

THIS PAGE BLANK (VISTO)